SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-1.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 1.rai.

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OM protein - protein search, using sw model

June 2, 2006, 19:12:07; Search time 12.7 Seconds Run on:

(without alignments)

103.383 Million cell updates/sec

Title: US-10-001-938-1

Perfect score: 76

Sequence: 1 QDYYEILGVSKTAEE 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

650591 seqs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Issued Patents AA:* Database :

> 1: /EMC Celerra SIDS3/ptodata/2/iaa/5_COMB.pep:* 2: /EMC Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:* 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:*

5: /EMC Celerra SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:* 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

/EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description		
1	76	100.0	131	2	US-09-553-498-4	Sequence 4, Appli		
2	76	100.0	131	2	US-09-618-869-4	Sequence 4, Appli		

3	76	100.0	380	2	US-09-489-039A-9011	Sequence	9011, Ap
4	76	100.0	399	2	US-09-553-498-2	Sequence	2, Appli
5	76	100.0	399	2	US-09-618-869-2	•	2, Appli
				-		•	
6	63	82.9	375	2	US-09-328-352-4984	_	4984, Ap
7	61	80.3	380	2	US-09-543-681A-5912	Sequence	5912, Ap
8	60	78.9	87	2	US-09-882-835-4	Sequence	4, Appli
9	58	76.3	372	2	US-09-270-767-45792		45792, A
				2		•	
10	55	72.4	332	=	US-09-882-835-2	•	2, Appli
11	55	72.4	373	2	US-09-710-279-890	Sequence	890, App
12	55	72.4	385	2	US-09-134-001C-3688	Sequence	3688, Ap
13	55	72.4	392	2	US-09-198-452A-48	Sequence	48, Appl
14	55	72.4	406	2	US-09-438-185A-34	-	34, Appl
				_		_	
15	55	72.4	747	2	US-09-999-833A-459	-	459, App
16	55	72.4	747	2	US-10-020-445A-459	Sequence	459, App
17	55	72.4	747	2	US-09-978-189-459	Sequence	459, App
18	55	72.4	747	2	US-10-017-085A-459	Sequence	
				3		-	
19	55	72.4	747		US-10-145-129A-459	Sequence	
20	55	72.4	747	3	US-10-013-929A-459	Sequence	459, App
21	55	72.4	747	3	US-10-013-917A-459	Sequence	459, App
22	54	71.1	376	3	US-10-375-010-22	Sequence	
				_	US-08-897-340-34		
23	54	71.1	438	1		Sequence	
24	54	71.1	438	2	US-09-252-329-34	Sequence	34, Appl
25	54	71.1	484	1	US-08-879-260-4	Sequence	4, Appli
26	54	71.1	484	2	US-09-231-529-4	Sequence	- -
27	54	71.1	484	2	US-08-977-816-4	•	4, Appli
				_		•	
28	54	71.1	484	2	US-09-639-207-5	-	5, Appli
29	53	69.7	407	2	US-09-540-236-2899	Sequence	2899, Ap
30	52	68.4	411	2	US-10-101-464A-982	Sequence	982, App
31	50	65.8	147	2	US-09-513-999C-6925	-	6925, Ap
32		65.8	368	2	US-09-861-451A-2	•	2, Appli
	50					_	
33	49	64.5	96	2	US-09-621-976-4045	•	4045, Ap
34	49	64.5	138	2	US-09-902-540-13689	Sequence	13689, A
35	49	64.5	223	2	US-09-658-644-4	Sequence	4, Appli
36	49	64.5	223	2	US-09-949-016-6832	-	6832, Ap
						_	•
37	49	64.5	267	2	US-09-949-016-11497	-	11497, A
38	49	64.5	387	2	US-09-908-992B-11	Sequence	11, Appl
39	49	64.5	414	2	US-09-908-992B-10	Sequence	10, Appl
40	49	64.5	453	2	US-09-908-992B-9	Seguence	9, Appli
41	49	64.5	453	2	US-09-908-992B-30	-	30, Appl
				_		——————————————————————————————————————	
42	49	64.5	480	2	US-09-908-992B-8	_	8, Appli
43	49	64.5	480	2	US-09-908-992B-12	Sequence	12, Appl
44	48	63.2	276	2	US-09-270-767-43364	Sequence	43364, A
45	48	63.2	381	2	US-09-252-991A-27174	Seguence	27174, A
46	48	63.2	419	1	US-08-686-417-3	•	3, Appli
				_			
47	48	63.2	504	2	US-09-231-529-6	-	6, Appli
48	48	63.2	504	2	US-08-977-816-6	Sequence	6, Appli
49	48	63.2	516	2	US-09-949-016-9654	Sequence	9654, Ap
50	47	61.8	138	2	US-09-270-767-42296	Sequence	42296, A
51	47	61.8	382	2	US-09-603-208A-40	•	40, Appl
				_			• • •
52	47	61.8	452	2	US-09-908-992B-29		29, Appl
53	47	61.8	479	2	US-09-908-992B-28	Sequence	28, Appl
54	47	61.8	508	2	US-09-639-207-1	Sequence	1, Appli
55	46	60.5	288	2	US-09-540-236-2885	-	2885, Ap
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56	46	60.5	330	1	US-08-868-288A-3		3, Appli
57	46	60.5	330	2	US-09-235-373-3	•	3, Appli
58	46	60.5	330	2	US-09-388-993-3	Sequence	3, Appli
59	46	60.5	330	2	US-09-501-714-3	Sequence	3, Appli
60	45	59.2	348	1	US-08-974-546-1	-	1, Appli
61	44	57.9	70	2	US-09-621-976-4403	•	4403, Ap
62	44	57.9	595	2	US-10-104-047-2714	-	2714, Ap
63	43	56.6	153	2	US-09-621-976-5129	Sequence	5129, Ap
						_	-

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-1.ra

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 1.rapbm.

<u>start</u>

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2006, 19:45:16; Search time 63.4 Seconds

(without alignments)

109.593 Million cell updates/sec

Title: US-10-001-938-1

Perfect score: 76

Sequence: 1 QDYYEILGVSKTAEE 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database: Published Applications AA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC_celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

- the number of negative mandicated by themes to been a

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
1	76	100.0	15	4	US-10-001-938-1	Sequence 1, Appli
2	76	100.0	376	4	US-10-369-493-689	Sequence 689, App
3	76	100.0	376	6	US-11-080-458-32	Sequence 32, Appl

4	68	89.5	378	4	US-10-369-493-386	Sequence	386, App
5	67	88.2	476	5	US-10-450-763-48130	Sequence	48130, A
6	62	81.6	370	6	US-11-097-143-5622	Sequence	5622, Ap
7	61	80.3	332	4	US-10-369-493-2834	Sequence	2834, Ap
8	60	78.9	87	4	US-10-145-586-48	Sequence	48, Appl
9	60	78.9	378	4	US-10-369-493-21305	-	21305, A
10	58	76.3	372	4	US-10-369-493-23206	•	23206, A
11	58	76.3	382	4	US-10-369-493-8065		8065, Ap
12	58	76.3	385	4	US-10-369-493-16754	-	16754, A
						•	·
13	57	75.0	187	4	US-10-424-599-165088	Sequence	•
14	57	75.0	201	5	US-10-732-923-9541	•	9541, Ap
15	57	75.0	288	4	US-10-369-493-8874	•	8874, Ap
16	57	75.0	322	4	US-10-369-493-20073	-	20073, A
17	57	75.0	367	4	US-10-369-493-8095	•	8095, Ap
18	56	73.7	317	4	US-10-156-761-14768	Sequence	14768, A
19	56	73.7	330	4	US-10-369-493-18826	Sequence	18826, A
20	56	73.7	330	4	US-10-369-493-19832	Sequence	19832, A
21	56	73.7	377	6	US-11-045-004-1504	Sequence	1504, Ap
22	56	73.7	420	4	US-10-369-493-591	•	591, App
23	56	73.7	420	4	US-10-767-701-46164	• • • • • • • • • • • • • • • • • • •	46164, A
24	56	73.7	422	4	US-10-425-115-332061	Sequence	*
				4	US-10-424-599-282287	Sequence	
25	56	73.7	427	_		•	•
26	56	73.7	429	4	US-10-425-115-209640	Sequence	•
27	56	73.7	429	6	US-11-096-568A-18416	•	18416, A
28	56	73.7	433	4	US-10-425-114-63266		63266, A
29	56	73.7	435	4	US-10-425-114-59462	-	59462, A
30	56	73.7	435	4	US-10-425-114-65366	•	65366, A
31	56	73.7	485	4	US-10-369-493-12487	Sequence	12487, A
32	55	72.4	110	3	US-09-764-868-1151	Sequence	1151, Ap
33	55	72.4	157	3	US-09-764-868-778	Sequence	778, App
34	55	72.4	208	4	US-10-767-701-41491	Sequence	41491, A
35	55	72.4	308	4	US-10-369-493-19014	Sequence	19014, A
36	55	72.4	319	4	US-10-282-122A-68006	_	68006, A
37	55	72.4	332	4	US-10-145-586-46	•	46, Appl
38	55	72.4	362	4	US-10-369-493-9305	-	9305, Ap
39	55 55	72.4	373	5	US-10-793-626-890	-	890, App
	55	72.4	374	6	US-11-098-686-10930	•	10930, A
40							·
41	55	72.4	379	4	US-10-369-493-7330	•	7330, Ap
42	55	72.4	380	4	US-10-369-493-4573	•	4573, Ap
43	55	72.4	392	4	US-10-289-762-48	•	48, Appl
44	55	72.4	420	4	US-10-437-963-128712	Sequence	•
45	55	72.4	747	3	US-09-978-295A-459	-	459, App
46	55	72.4	747	3	US-09-938-418-9	_	9, Appli
47	55	72.4	747	3	US-09-978-697-459	_	459, App
48	55	72.4	747	3	US-09-978-192A-459	Sequence	459, App
49	55	72.4	747	3	US-09-999-832A-459	Sequence	459, App
50	55	72.4	747	3	US-09-978-189-459	Sequence	459, App
51	55	72.4	747	3	US-09-978-608A-459	-	459, App
52	55	72.4	747	3	US-09-978-585A-459	_	459, App
53	55	72.4	747	3	US-09-978-191A-459	-	459, App
54	55	72.4	747	3	US-09-978-403A-459	-	459, App
55 55	55	72.4	747	3	US-09-978-564A-459	_	459, App
						-	_ •
56	55	72.4	747	3	US-09-999-833A-459	-	459, App
57	55	72.4	747	3	US-09-981-915A-459	_	459, App
58	55	72.4	747	3	US-09-978-824-459	_	459, App
59	55	72.4	747	3	US-09-918-585A-459	-	459, App
60	55	72.4	747	3	US-09-999-834A-459	-	459, App
61	55	72.4	747	3	US-09-978-423A-459	Sequence	459, App
62	55	72.4	747	3	US-09-978-193A-459	Sequence	459, App
63	55	72.4	747	3	US-09-999-830A-459	Sequence	459, App
64	55	72.4	747	3	US-09-978-757A-459	Sequence	459, App
						-	

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-1.rapbn.

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SCORE FAQ

Comments / **Suggestions**

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OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:44:08; Search time 3.1 Seconds

(without alignments)

55.960 Million cell updates/sec

Title:

US-10-001-938-1

Perfect score: 76

1 QDYYEILGVSKTAEE 15

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched:

Sequence:

58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New:*

/EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 NEW PUB.pep:*

4: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US08 NEW_PUB.pep:*

5: /EMC Celerra SIDS3/ptodata/2/pubpaa/PCT NEW PUB.pep:*

6: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US10 NEW PUB.pep:*

/EMC Celerra SIDS3/ptodata/2/pubpaa/US11 NEW PUB.pep:*

/EMC Celerra SIDS3/ptodata/2/pubpaa/US60 NEW PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

No.	Score	Match	Length	DB	ID	Description
1	 76	100.0	15	6	US-10-490-949-2	Sequence 2, Appli
2	58	76.3	367	6	US-10-953-349-1406	Sequence 1406, Ap
3	58	76.3	456	6	US-10-953-349-1405	Sequence 1405, Ap
4	52	68.4	420	6	US-10-953-349-13709	Sequence 13709, A
5	50	65.8	380	6	US-10-953-349-7175	Sequence 7175, Ap
6	50	65.8	389	7	US-11-122-986-185	Sequence 185, App
7	50	65.8	389	7	US-11-122-986-187	Sequence 187, App
8	50	65.8	391	6	US-10-953-349-7174	Sequence 7174, Ap
9	50	65.8	417	6	US-10-953-349-16377	Sequence 16377, A
10	50	65.8	442	6	US-10-953-349-7173	Sequence 7173, Ap
11	49	64.5	465	6	US-10-953-349-8070	Sequence 8070, Ap
12	49	64.5	473	6	US-10-953-349-8069	Sequence 8069, Ap
13	49	64.5	482	6	US-10-953-349-8068	Sequence 8068, Ap
14	48	63.2	504	6	US-10-511-937-2547	Sequence 2547, Ap
15	47	61.8	391	6	US-10-953-349-7627	Sequence 7627, Ap
16	46	60.5	419	6	US-10-953-349-1054	Sequence 1054, Ap
17	43	56.6	379	6	US-10-953-349-11645	Sequence 11645, A
18	42	55.3	336	6	US-10-953-349-33810	Sequence 33810, A
19	42	55.3	430	6	US-10-953-349-33809	Sequence 33809, A
20	41	53.9	199	6	US-10-953-349-9116	Sequence 9116, Ap
21	41	53.9	248	6	US-10-953-349-9115	Sequence 9115, Ap
22	41	53.9	273	6	US-10-953-349-4464	Sequence 4464, Ap
23	41	53.9	349	6	US-10-953-349-948	Sequence 948, App
24	41	53.9	349	6	US-10-953-349-4463	Sequence 4463, Ap
25	41	53.9	367	6	US-10-953-349-4462	Sequence 4462, Ap
26	40	52.6	15	6	US-10-490-949-19	Sequence 19, Appl
27	39	51.3	305	6	US-10-953-349-23847	Sequence 23847, A
28	39	51.3	583	6	US-10-953-349-35418	Sequence 35418, A
29	39	51.3	630	6	US-10-953-349-35417	Sequence 35417, A
30 31	39 38	51.3 50.0	750 333	6 6	US-10-511-937-2413 US-10-953-349-2863	Sequence 2413, Ap
32	38	50.0	333	6	US-10-953-349-2865	Sequence 2863, Ap Sequence 11247, A
33	38	50.0	397	7	US-11-293-697-3837	Sequence 3837, Ap
34	38	50.0	426	7	US-11-293-697-4751	Sequence 4751, Ap
35	37	48.7		6	US-10-490-949-20	Sequence 20, Appl
36	37	48.7	95	6	US-10-953-349-31080	Sequence 31080, A
37	37	48.7	156	6	US-10-953-349-5018	Sequence 5018, Ap
38	37	48.7	365	7	US-11-180-275A-5	Sequence 5, Appli
39	37	48.7	408	6	US-10-953-349-32513	Sequence 32513, A
40	37	48.7	496	6	US-10-953-349-32512	Sequence 32512, A
41	37	48.7	524	6	US-10-953-349-32511	Sequence 32511, A
42	36	47.4	15	6	US-10-490-949-18	Sequence 18, Appl
43	35.5	46.7	283	6	US-10-953-349-23347	Sequence 23347, A
44	35.5	46.7	301	6	US-10-953-349-23346	Sequence 23346, A
45	35.5	46.7	353	6	US-10-953-349-23345	Sequence 23345, A
46	35	46.1	253	6	US-10-953-349-5910	Sequence 5910, Ap
47	35	46.1	260	7	US-11-293-697-2489	Sequence 2489, Ap
48	35	46.1	268	6	US-10-953-349-5909	Sequence 5909, Ap
49	35	46.1	277	6	US-10-953-349-24470	Sequence 24470, A
50	35	46.1	292	6	US-10-953-349-24469	Sequence 24469, A
51	35	46.1	300	6	US-10-953-349-24468	Sequence 24468, A
52	35	46.1	302	6	US-10-953-349-5908	Sequence 5908, Ap
53	35	46.1	332	7	US-11-297-134-48	Sequence 48, Appl
54	35	46.1	335	6	US-10-953-349-2182	Sequence 2182, Ap
55	35	46.1	339	6	US-10-953-349-12422	Sequence 12422, A
56	35	46.1	343	6	US-10-953-349-2181	Sequence 2181, Ap
57	35	46.1	431	6	US-10-953-349-22612	Sequence 22612, A
58 50	35	46.1	557	7	US-11-293-697-4833	Sequence 4833, Ap
59	34	44.7	138	6	US-10-953-349-25278	Sequence 25278, A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-10

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-0(10.rai.

<u>start</u>

Go Back to pre

GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2006, 19:12:07; Search time 12.7 Seconds

(without alignments)

103.383 Million cell updates/sec

Title: US-10-001-938-10

Perfect score: 78

Sequence: 1 KDYYQTLGLARGASD 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database: Issued Patents AA:*

1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length :	DB	ID	Description		
1	78	100.0	340	1	US-08-974-546-5	Sequence 5, Appli		
2	78	100.0	340	2	US-09-949-016-6691	Sequence 6691, Ap		

3	78	100.0	363	2	US-09-949-016-8899	Sequence	8899, Ap
4	56	71.8	138	2	US-09-270-767-42296	Sequence	42296, A
5	56	71.8	508	2	US-09-639-207-1	Seguence	1, Appli
6	54	69.2	334	3	US-10-429-223-3	_	3, Appli
7	54	69.2	337	2	US-09-665-479A-8	_	8, Appli
		66.7		_		_	
8	52		391	2	US-09-902-540-11110	-	11110, A
9	51	65.4	381	2	US-09-252-991A-27174	_	27174, A
10	50	64.1	364	2	US-09-270-767-43685	Sequence	43685, A
11	50	64.1	375	2	US-09-328-352-4984	Sequence	4984, Ap
12	50	64.1	376	3	US-10-375-010-22	Sequence	22, Appl
13	48	61.5	147	2	US-09-513-999C-6925	•	6925, Ap
14	48	61.5	348	1	US-08-974-546-1	-	1, Appli
15		61.5	347	2	US-09-908-992B-11	-	
	48					_	11, Appl
16	48	61.5	414	2	US-09-908-992B-10	-	10, Appl
17	48	61.5	453	2	US-09-908-992B-9	•	9, Appli
18	48	61.5	453	2	US-09-908-992B-30	Sequence	30, Appl
19	48	61.5	480	2	US-09-908-992B-8	Sequence	8, Appli
20	48	61.5	480	2	US-09-908-992B-12	Sequence	12, Appl
21	47	60.3	452	2	US-09-908-992B-29	-	29, Appl
22	47	60.3	479	2	US-09-908-992B-28	_	28, Appl
				_		_	• • •
23	47	60.3	554	2	US-09-167-299-4	_	4, Appli
24	46	59.0	372	2	US-09-270-767-45792	•	45792, A
25	46	59.0	438	1	US-08-897-340-34	Sequence	34, Appl
26	46	59.0	438	2	US-09-252-329-34	Sequence	34, Appl
27	46	59.0	484	1	US-08-879-260-4	Sequence	4, Appli
28	46	59.0	484	2	US-09-231-529-4	•	4, Appli
29	46	59.0	484	2	US-08-977-816-4	_	4, Appli
				2	US-09-639-207-5	-	5, Appli
30	46	59.0	484			•	
31	45	57.7	153	2	US-09-621-976-5129	•	5129, Ap
32	45	57. 7	276	2	US-09-270-767-43364	•	43364, A
33	44	56.4	87	2	US-09-882-835-4	Sequence	4, Appli
34	43	55.1	261	2	US-09-902-540-15463	Sequence	15463, A
35	43	55.1	330	1	US-08-868-288A-3	Sequence	3, Appli
36	43	55.1	330	2	US-09-235-373-3		3, Appli
37	43	55.1	330	2	US-09-388-993-3	-	3, Appli
38	43	55.1	330	2	US-09-501-714-3	_	3, Appli
						•	
39	43	55.1	373	2	US-09-710-279-890	-	890, App
40	43	55.1	385	2	US-09-134-001C-3688	•	3688, Ap
41	43	55.1	395	2	US-09-712-363-164	_	164, App
42	43	55.1	493	2	US-09-613-303-19	Sequence	19, Appl
43	43	55.1	493	2	US-10-267-311-19	Sequence	19, Appl
44	42	53.8	130	2	US-09-252-991A-29173	Sequence	29173, A
45	42	53.8	320	2	US-09-328-352-7937	•	7937, Ap
46	41	52.6	70	2	US-09-621-976-4403	•	4403, Ap
47	41	52.6	197	2	US-10-094-749-2714	•	2714, Ap
				_		•	
48	41	52.6	358	1	US-08-868-288A-1	-	1, Appli
49	41	52.6	358	2	US-09-235-373-1	•	1, Appli
50	41	52.6	358	2	US-09-388-993-1	Sequence	1, Appli
51	41	52.6	358	2	US-09-991-181-148	Sequence	148, App
52	41	52.6	358	2	US-09-501-714-1	Sequence	1, Appli
53	41	52.6	358	2	US-09-990-444-148	•	148, App
54	41	52.6	358	2	US-09-997-333-148	-	148, App
				2	US-09-992-598-148		
55 56	41	52.6	358				148, App
56	41	52.6	358	2	US-09-989-735-148	-	148, App
5 7	41	52.6	358	3	US-09-989-726-148	-	148, App
58	41	52.6	358	3	US-09-997-514-148	•	148, App
59	41	52. 6.	358	3	US-09-989-728-148	Sequence	148, App
60	41	52.6	358	3	US-09-997-349-148	Sequence	148, App
61	41	52.6	358	3	US-09-997-653-148	-	148, App
62	41	52.6	358	3	US-09-989-293A-148	_	148, App
63	41	52.6	380	2	US-09-543-681A-5912	•	5912, Ap
0.5	3.7	52.0	300	_	00 00 010 00IR 00IZ	Dequemoc	, 1.P

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938 10.rapbm.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 10.rapbm.

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Go Back to pro

GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:45:16; Search time 63.4 Seconds

(without alignments)

109.593 Million cell updates/sec

Title:

US-10-001-938-10

Perfect score: 78

1 KDYYQTLGLARGASD 15

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched:

Sequence:

2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters:

2097797

Minimum DB seg length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA Main: *

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC_Celerra SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		8	
Result		Query	
No.	Score	Match	Le

ength DB ID Description

1 78 100.0 15 4 US-10-001-938-10 Sequence 10, Appl

2	78	100.0	70	6	US-11-047-063-1	Sequence	1, Appli
3	78	100.0	340	4	US-10-116-275-134	Sequence	134, App
4	78	100.0	340	4	US-10-116-275-135	-	135, App
	78	100.0	340	5			
5				_	US-10-871-388-5	-	5, Appli
6	78	100.0	340	5	US-10-792-571-16	-	16, Appl
7	78	100.0	340	6	US-11-047-063-2	Sequence	2, Appli
8	78	100.0	377	5	US-10-450-763-48884	Sequence	48884, A
9	64	82.1	375	4	US-10-369-493-15859	Sequence	15859, A
10	64	82.1	376	4	US-10-369-493-15487		15487, A
		80.8	258	3		•	·
11	63			-	US-09-764-868-1161	Sequence	•
12	63	80.8	387	4	US-10-408-765A-2002	Sequence	•
13	59	75.6	288	4	US-10-369-493-8874	Sequence	8874, Ap
14	56	71.8	344	6	US-11-087-099-977	Sequence	977, App
15	56	71.8	474	4	US-10-437-963-139809	Sequence	139809,
16	56	71.8	474	6	US-11-087-099-7037	-	7037, Ap
17	56	71.8	474	6	US-11-087-099-7585	-	7585, Ap
				-		-	· · · · · · · · · · · · · · · · · · ·
18	56	71.8	508	4	US-10-465-217-1	-	1, Appli
19	56	71.8	508	6	US-11-097-143-9177	Sequence	9177, Ap
20	55	70.5	111	4	US-10-425-115-293770	Sequence	293770,
21	55	70.5	203	4	US-10-425-114-60728	Sequence	60728, A
22	55	70.5	336	4	US-10-425-115-295968	Sequence	•
23	55	70.5	336	6	US-11-096-568A-20392	_	20392, A
				_		•	· •
24	55	70.5	345	5	US-10-739-930-10685	_	10685, A
25	55	70.5	371	4	US-10-425-114-47700	Sequence	47700, A
26	55	70.5	379	4	US-10-369-493-7330	Sequence	7330, Ap
27	55	70.5	380	4	US-10-369-493-4573	Sequence	4573, Ap
28	55	70.5	388	4	US-10-425-114-46994	•	46994, A
29	55	70.5	388	4	US-10-425-114-58689	•	58689, A
				_		-	
30	55	70.5	390	4	US-10-425-114-52134	•	52134, A
31	55	70.5	414	6	US-11-096-568A-20391	•	20391, A
32	54	69.2	158	4	US-10-425-114-48912	Sequence	48912, A
33	54	69.2	193	3	US-09-925-301-983	Sequence	983, App
34	54	69.2	326	4	US-10-425-115-300448	Sequence	300448,
35	54	69.2	334	4	US-10-429-223-3	-	3, Appli
36	54	69.2	337	4	US-10-788-792-162	-	162, App
37	54	69.2	356	4	US-10-437-963-126176	Sequence	•
38	54	69.2	378	4	US-10-369-493-8450	-	8450, Ap
39	52	66.7	310	4	US-10-369-493-4694	Sequence	4694, Ap
40	52	66.7	329	4	US-10-282-122A-49700	Sequence	49700, A
41	52	66.7	368	4	US-10-369-493-19421	Sequence	19421, A
42	52	66.7	374	4	US-10-369-493-13658	Sequence	13658, A
43	51	65.4	88	4	US-10-425-115-294867	Sequence	
						•	134, App
44	51	65.4	334	4	US-10-161-051-134		
45	51	65.4	334	6	US-11-097-143-22242	•	22242, A
46	51	65.4	336	6	US-11-096-568A-25864	Sequence	25864, A
47	51	65.4	387	4	US-10-425-114-60791	Sequence	60791, A
48	51	65.4	430	6	US-11-096-568A-25863	Sequence	25863, A
49	51	65.4	513	6	US-11-097-143-11568	•	11568, A
50	50	64.1	332	4	US-10-369-493-2834	•	2834, Ap
						•	•
51	50	64.1	342	6	US-11-097-143-3567	•	3567, Ap
52	50	64.1	353	6	US-11-097-143-15813	•	15813, A
53	50	64.1	362	4	US-10-369-493-9305	Sequence	9305, Ap
54	50	64.1	365	4	US-10-369-493-18240	Sequence	18240, A
55	50	64.1	370	6	US-11-097-143-5622	Sequence	5622, Ap
56	50	64.1	376	4	US-10-375-010-22	•	22, Appl
57	50	64.1	376	6	US-11-232-406A-22	-	22, Appl
						-	• •
58	49	62.8	66	6	US-11-039-722-7	-	7, Appli
59	49	62.8	73	4	US-10-425-115-208567		208567,
60	49	62.8	128	6	US-11-097-143-15807	-	15807, A
61	49	62.8	271	6	US-11-087-099-7430	Sequence	7430, Ap
62	49	62.8	317	4	US-10-156-761-14768	Sequence	14768, A
-			-			•	•

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-10.rapbn.

Score Home Page Retrieve Application

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Overview

SCORE FAQ Comments / Suggestions

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-001-938-10.rapbn.

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OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:44:08; Search time 3.1 Seconds

(without alignments)

55.960 Million cell updates/sec

Title:

US-10-001-938-10

Perfect score: 78

Sequence: 1 KDYYQTLGLARGASD 15

Scoring table: B

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters:

58871

Minimum DB seg length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New: *

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 NEW PUB.pep:*

4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

No.	Score	Match	Length	DB	ID	Description
1	78	100.0	15	6	US-10-490-949-19	Sequence 19, Appl
2	64	82.1	389	7	US-11-122-986-185	Sequence 185, App
3	64	82.1	389	7	US-11-122-986-187	Sequence 187, App
4	51	65.4	336	6	US-10-953-349-33810	Sequence 33810, A
5	51	65.4	430	6	US-10-953-349-33809	Sequence 33809, A
6	45	57.7	367	6	US-10-953-349-1406	Sequence 1406, Ap
7	45	57.7	456	6	US-10-953-349-1405	Sequence 1405, Ap
8	44	56.4	465	6	US-10-953-349-8070	Sequence 8070, Ap
9	44	56.4	473	6	US-10-953-349-8069	Sequence 8069, Ap
10	44	56.4	482	6	US-10-953-349-8068	Sequence 8068, Ap
11	42	53.8	273	6	US-10-953-349-4464	Sequence 4464, Ap
12	42	53.8	349	6	US-10-953-349-4463	Sequence 4463, Ap
13	42	53.8	367	6	US-10-953-349-4462	Sequence 4462, Ap
14	41	52.6	199	6	US-10-953-349-9116	Sequence 9116, Ap
15	41	52.6	248	6	US-10-953-349-9115	Sequence 9115, Ap
16	41	52.6	281	6	US-10-953-349-18417	Sequence 18417, A
17	41	52.6	351	6	US-10-953-349-18416	Sequence 18416, A
18	41	52.6	504	6	US-10-511-937-2547	Sequence 2547, Ap
19	40	51.3	15	6	US-10-490-949-2	Sequence 2, Appli
20	40	51.3	260	7	US-11-293-697-2489	Sequence 2489, Ap
21	39	50.0	357	6	US-10-953-349-2656	Sequence 2656, Ap
22	39	50.0	364	6	US-10-953-349-2655	Sequence 2655, Ap
23	39	50.0	372	6	US-10-953-349-2654	Sequence 2654, Ap
24	39	50.0	380	6	US-10-953-349-7175	Sequence 7175, Ap
25	39	50.0	391	6	US-10-953-349-7174	Sequence 7174, Ap
26	39	50.0	442	6	US-10-953-349-7173	Sequence 7173, Ap
27	39	50.0	586	6	US-10-953-349-38530	Sequence 38530, A
28 29	39	50.0	627 15 <i>6</i>	6	US-10-953-349-38529	Sequence 38529, A
30	38 38	48.7 48.7	156 169	6 6	US-10-370-959-126 US-10-953-349-27713	Sequence 126, App
31	38	48.7	172	6	US-10-953-349-27713	Sequence 27713, A Sequence 10393, A
32	38	48.7	324	6	US-10-953-349-10393	Sequence 10393, A
33	37	47.4	161	6	US-10-953-349-15793	Sequence 15793, A
34	37	47.4	182	6	US-10-953-349-15792	Sequence 15792, A
35	37	47.4	295	7	US-11-122-986-275	Sequence 275, App
36	37	47.4	295	7	US-11-122-986-277	Sequence 277, App
37	37	47.4	417	6	US-10-953-349-16377	Sequence 16377, A
38	37	47.4	420	6	US-10-953-349-13709	Sequence 13709, A
39	36	46.2	126	6	US-10-953-349-2572	Sequence 2572, Ap
40	36	46.2	188	6	US-10-953-349-17319	Sequence 17319, A
41	36	46.2	191	6	US-10-953-349-2571	Sequence 2571, Ap
42	36	46.2	230	6	US-10-953-349-2570	Sequence 2570, Ap
43	36	46.2	267	6	US-10-953-349-17318	Sequence 17318, A
44	36	46.2	310	6	US-10-953-349-21677	Sequence 21677, A
45	36	46.2	311	6	US-10-953-349-17317	Sequence 17317, A
46	36	46.2	311	6	US-10-953-349-21676	Sequence 21676, A
47	36	46.2	333	6	US-10-953-349-2863	Sequence 2863, Ap
48	36	46.2	333	6	US-10-953-349-11247	Sequence 11247, A
49	36	46.2	456	6	US-10-953-349-21675	Sequence 21675, A
50	35	44.9	317	6	US-10-953-349-11729	Sequence 11729, A
51	35	44.9	497	6	US-10-953-349-480	Sequence 480, App
52	35	44.9	498	6	US-10-953-349-479	Sequence 479, App
53	35	44.9	500	6	US-10-953-349-478	Sequence 478, App
54	34	43.6	95	6	US-10-953-349-31080	Sequence 31080, A
55	34	43.6	190	6	US-10-953-349-28214	Sequence 28214, A
56	34	43.6	191	6	US-10-953-349-28213	Sequence 28213, A
57 50	34	43.6	335	6	US-10-953-349-2182	Sequence 2182, Ap
58 50	34	43.6	343	6		Sequence 2181, Ap
59	34	43.6	344	6	US-10-953-349-3691	Sequence 3691, Ap

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-11

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 11.rai.

<u>start</u>

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OM protein - protein search, using sw model

June 2, 2006, 19:37:25; Search time 14.6053 Seconds Run on:

(without alignments)

89.896 Million cell updates/sec

Title: US-10-001-938-11

Perfect score: 80

1 TTYYDVLGVKPNATQ 15 Sequence:

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

650591 seqs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

> /EMC Celerra SIDS3/ptodata/2/iaa/5_COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/iaa/PCTUS COMB.pep:* 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

/EMC Celerra SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length DB ID			Description		
1	80	100.0	102	2	US-09-513-999C-5137	Sequence 5137, Ap		
2	80	100.0	127	2	US-09-370-838-199	Sequence 199, App		

_				_		_	
3	80	100.0	127	2	US-09-854-133-199	Sequence	199, App
4	80	100.0	397	1	US-08-868-288A-5	Sequence	5, Appli
5	80	100.0	397	2	US-09-235-373-5	Sequence	5, Appli
6	80	100.0	397	2	US-09-388-993-5	Sequence	5, Appli
7	80	100.0	397	2	US-09-919-039-178	_	178, App
8	80	100.0	397	2	US-09-538-092-1052	•	1052, Ap
9	80	100.0	397	2	US-09-501-714-5	•	5, Appli
	59	73.8	397	3	US-10-429-223-2	-	
10				_			2, Appli
11	59	73.8	397	3	US-10-429-223-4	-	4, Appli
12	52	65.0	397	2	US-09-248-796A-17628	•	17628, A
13	51	63.7	482	2	US-09-538-092-454	Sequence	454, App
14	48	60.0	115	2	US-09-248-796A-16551	Sequence	16551, A
15	47	58.8	99	2	US-09-248-796A-19786	Sequence	19786, A
16	46	57.5	75	2	US-09-513-999C-6016	Sequence	6016, Ap
17	46	57.5	419	1	US-08-686-417-3	Sequence	3, Appli
18	44	55.0	73	2	US-09-513-999C-7608	-	7608, Ap
19	44	55.0	96	2	US-09-621-976-4045	_	4045, Ap
20	44	55.0	223	2	US-09-658-644-4	•	4, Appli
21	44	55.0	223	2	US-09-949-016-6832	•	6832, Ap
22	44	55.0	267	2	US-09-949-016-11497	•	
				_		•	11497, A
23	44	55.0	382	2	US-09-603-208A-40	•	40, Appl
24	44	55.0	387	2	US-09-908-992B-11	-	11, Appl
25	44	55.0	414	2	US-09-908-992B-10	_	10, Appl
26	44	55.0	452	2	US-09-908-992B-29	Sequence	29, Appl
27	44	55.0	453	2	US-09-908-992B-9	Sequence	9, Appli
28	44	55.0	453	2	US-09-908-992B-30	Sequence	30, Appl
29	44	55.0	479	2	US-09-908-992B-28	Sequence	28, Appl
30	44	55.0	480	2	US-09-908-992B-8	Sequence	8, Appli
31	44	55.0	480	2	US-09-908-992B-12	-	12, Appl
32	43	53.8	158	2	US-09-248-796A-19793	-	19793, A
33	43	53.8	380	2	US-09-540-236-2987	•	2987, Ap
34	43	53.8	504	2	US-09-231-529-6	-	6, Appli
35	43	53.8	504	2	US-08-977-816-6		6, Appli
36	43	53.8	515	2	US-09-248-796A-19787	_	· • •
37				2		-	19787, A
	43	53.8	516		US-09-949-016-9654	-	9654, Ap
38	42	52.5	281	2	US-09-902-540-15871	•	15871, A
39	41	51.2	268	2	US-09-270-767-39827	•	39827, A
40	41	51.2	268	2	US-09-270-767-55044	•	55044, A
41	41	51.2	352	1	US-08-472-534-6	Sequence	6, Appli
42	41	51.2	378	2	US-09-583-110-4647	Sequence	4647, Ap
43	41	51.2	379	2	US-09-107-433-3487	Sequence	3487, Ap
44	41	51.2	438	1	US-08-897-340-34	Sequence	34, Appl
45	41	51.2	438	2	US-09-252-329-34	Sequence	34, Appl
46	41	51.2	484	1	US-08-879-260-4	Sequence	4, Appli
47	41	51.2	484	2	US-09-231-529-4	Sequence	4, Appli
48	41	51.2	484	2	US-08-977-816-4	_	4, Appli
49	41	51.2	484	2	US-09-639-207-5	•	5, Appli
50	40	50.0	87	2	US-09-882-835-4	•	4, Appli
51	40	50.0	147	2	US-09-270-767-33311	_	33311, A
52	40	50.0	147	2	US-09-270-767-48528	•	48528, A
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53	40	50.0	276	2	US-09-270-767-43364	•	43364, A
54	40	50.0	373	2	US-09-710-279-890	-	890, App
55	40	50.0	376	3	US-10-375-010-22	•	22, Appl
56	40	50.0	385	2	US-09-134-001C-3688	•	3688, Ap
57	40	50.0	400	2	US-09-489-039A-13012	•	13012, A
58	39	48.8	236	2	US-09-270-767-42239	•	42239, A
59	39	48.8	264	2	US-09-134-000C-6709	_	6709, Ap
60	39	48.8	284	3	US-09-191-651-10	Sequence	10, Appl
61	39	48.8	320	2	US-09-543-681A-7884	Sequence	7884, Ap
62	39	48.8	320	2	US-09-248-796A-17629	Sequence	17629, A
63	39	48.8	330	1	US-08-868-288A-3	Sequence	3, Appli
						-	-

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938 11.rapbm.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 11.rapbm.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

June 2, 2006, 19:58:51; Search time 63.3553 Seconds Run on:

(without alignments)

109.671 Million cell updates/sec

Title: US-10-001-938-11

Perfect score: 80

Sequence: 1 TTYYDVLGVKPNATQ 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA Main:*

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A PUBCOMB.pep:*

5: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:* 6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11 PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

용 Result Query No. Score Match Length DB ID Description 1 80 100.0 15 4 US-10-001-938-11 Sequence 11, Appl

_				_			
2	80	100.0	127	3	US-09-738-973-199	Sequence	199, App
3	80	100.0	127	3	US-09-854-133-199	Sequence	199, App
4	80	100.0	127	4	US-10-144-649A-199	Sequence	
5	80	100.0	397	3	US-09-919-039-178	-	178, App
	80	100.0	397	5	US-10-473-127-1138	-	
6				_		-	1138, Ap
7	80	100.0	397	5	US-10-473-127-1139	_	1139, Ap
8	80	100.0	397	5	US-10-473-127-1140	Sequence	1140, Ap
9	80	100.0	397	5	US-10-473-127-1143	Sequence	1143, Ap
10	80	100.0	397	5	US-10-473-127-1144	Sequence	1144, Ap
11	80	100.0	397	5	US-10-473-127-1145	•	1145, Ap
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12	80	100.0	397	5	US-10-756-149-4727	-	4727, Ap
13	80	100.0	397	5	US-10-631-467-559	Sequence	559, App
14	80	100.0	397	5	US-10-631-467-1386	Sequence	1386, Ap
15	80	100.0	397	5	US-10-878-556A-155	Sequence	155, App
16	80	100.0	408	5	US-10-450-763-40099	•	40099, A
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17	67	83.8	403	6	US-11-097-143-24405	•	24405, A
18	67	83.8	403	6	US-11-097-143-41904	Sequence	41904, A
19	61	76.2	26	5	US-10-862-195-1870	Sequence	1870, Ap
20	60	75.0	390	4	US-10-425-115-236372	Sequence	236372,
21	60	75.0	391	4	US-10-767-701-45927	•	45927, A
22	60	75.0	395	4	US-10-425-114-63467	•	·
				_		Sequence	•
23	60	75.0	398	6	US-11-096-568A-31579	•	31579, A
24	59	73.8	121	4	US-10-437-963-151256	Sequence	151256,
25	59	73.8	313	4	US-10-437-963-183087	Sequence	183087,
26	59	73.8	397	4	US-10-108-260A-3837	•	3837, Ap
27	59	73.8	397	4	US-10-429-223-2	•	2, Appli
				_		-	
28	59	73.8	397	4	US-10-429-223-4	-	4, Appli
29	59	73.8	426	4	US-10-108-260A-4751	•	4751, Ap
30	58	72.5	145	4	US-10-767-701-55698	Sequence	55698, A
31	54	67.5	123	4	US-10-425-115-239628	Sequence	239628,
32	53	66.2	51	4	US-10-424-599-274377	Sequence	274377,
33	53	66.2	107	4	US-10-767-701-48835	•	48835, A
34	53	66.2	208	4	US-10-767-701-41491	•	41491, A
				_		•	•
35	52	65.0	60	4	US-10-424-599-160806	Sequence	· · · · · · · · · · · · · · · · · · ·
36	52	65.0	155	4	US-10-425-115-220433	Sequence	•
37	52	65.0	217	4	US-10-424-599-271036	Sequence	271036,
38	52	65.0	410	4	US-10-424-599-271035	Sequence	271035,
39	52	65.0	417	4	US-10-424-599-271037	Sequence	271037.
40	52	65.0	442	4	US-10-437-963-196211	Sequence	•
41	51	63.7	212	4		•	·
				_	US-10-425-115-309309	Sequence	•
42	51	63.7	420	4	US-10-437-963-128712	Sequence	•
43	49	61.3	47	4	US-10-424-599-188229	Sequence	188229,
44	49	61.3	80	4	US-10-424-599-205273	Sequence	205273,
45	49	61.3	121	4	US-10-425-115-244815	Sequence	244815,
46	49	61.3	386	4	US-10-425-115-191974	Sequence	·
47	49	61.3	391	4	US-10-425-114-63066	•	63066, A
						_	
48	49	61.3	391	4	US-10-425-114-63612	•	63612, A
49	49	61.3	420	4	US-10-424-599-257607	Sequence	257607,
50	48	60.0	35	4	US-10-425-115-220432	Sequence	220432,
51	48	60.0	64	4	US-10-424-599-247165	Sequence	247165,
52	48	60.0	85	4	US-10-425-115-327744	Sequence	
53	48	60.0	94	4	US-10-425-115-336842	Sequence	•
				-		-	
54	48	60.0	148	4	US-10-767-701-32479	-	32479, A
55	48	60.0	185	4	US-10-767-701-44451	•	44451, A
56	48	60.0	195	6	US-11-096-568A-16365	Sequence	16365, A
57	48	60.0	197	4	US-10-425-114-61161	Sequence	61161, A
58	48	60.0	200	4	US-10-425-115-298432	Sequence	298432.
59	48	60.0	241	3	US-09-765-205-32	_	32, Appl
60	48	60.0	241	5	US-10-347-669-32	_	32, Appl
				-		•	• • •
61 62	48	60.0	343	4	US-10-425-115-228357	Sequence	•
62	48	60.0	344	4	US-10-425-114-73013	sequence	73013, A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-11.rapbn.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:45:07; Search time 3.55263 Seconds

(without alignments)

48.831 Million cell updates/sec

Title:

US-10-001-938-11

Perfect score: 80

Sequence:

1 TTYYDVLGVKPNATQ 15

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

58871 segs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New:*

/EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra SIDS3/ptodata/2/pubpaa/US08 NEW PUB.pep:*

5: /EMC Celerra SIDS3/ptodata/2/pubpaa/PCT NEW PUB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

/EMC Celerra SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

/EMC Celerra SIDS3/ptodata/2/pubpaa/US60 NEW PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

No.	Score	Match	Length	DB	ID	Description
1	80	100.0	15	6	US-10-490-949-20	Sequence 20, Appl
2	59	73.8	397	7	US-11-293-697-3837	Sequence 3837, Ap
3	59	73.8	426	7	US-11-293-697-4751	Sequence 4751, Ap
4	57	71.2	379	6	US-10-953-349-11645	Sequence 11645, A
5	56	70.0	391	6	US-10-953-349-7627	Sequence 7627, Ap
6	49	61.3	420	6	US-10-953-349-13709	Sequence 13709, A
7	47	58.8	380	6	US-10-953-349-7175	Sequence 7175, Ap
8	47	58.8	391	6	US-10-953-349-7174	Sequence 7174, Ap
9	47	58.8	417	6	US-10-953-349-16377	Sequence 16377, A
10	47	58.8	442	6	US-10-953-349-7173	Sequence 7173, Ap
11	44	55.0	339	6	US-10-953-349-12422	Sequence 12422, A
12	43	53.8	190	6	US-10-953-349-28214	Sequence 28214, A
13	43	53.8	191	6	US-10-953-349-28213	Sequence 28213, A
14	43	53.8	504	6	US-10-511-937-2547	Sequence 2547, Ap
15	42	52.5	367	6	US-10-953-349-1406	Sequence 1406, Ap
16	42	52.5	456	6	US-10-953-349-1405	Sequence 1405, Ap
17	41	51.2	95	6	US-10-953-349-31080	Sequence 31080, A
18	41	51.2	333	6	US-10-953-349-2863	Sequence 2863, Ap
19	41	51.2	333	6	US-10-953-349-11247	Sequence 11247, A
20	40	50.0	199	6	US-10-953-349-9116	Sequence 9116, Ap
21	40	50.0	248	6	US-10-953-349-9115	Sequence 9115, Ap
22	40	50.0	548	6	US-10-953-349-17843	Sequence 17843, A
23	39	48.8	191	6	US-10-953-349-34839	Sequence 34839, A
24	39	48.8	193	6	US-10-953-349-34838	Sequence 34838, A
25	39	48.8	196	6	US-10-953-349-34837	Sequence 34837, A
26	39	48.8	198	6	US-10-953-349-31537	Sequence 31537, A
27	39	48.8	223	6	US-10-953-349-9541	Sequence 9541, Ap
28	39	48.8	226	6	US-10-953-349-9540	Sequence 9540, Ap
29	39	48.8	282	6	US-10-953-349-31536	Sequence 31536, A
30	39	48.8	331	6	US-10-953-349-31535	Sequence 31535, A
31	38	47.5	138	6	US-10-953-349-39107	Sequence 39107, A
32 33	38	47.5 47.5	156	6 6	US-10-953-349-5018	Sequence 5018, Ap
33 34	38 38	47.5	174 583	6	US-10-953-349-39106 US-10-953-349-35418	Sequence 39106, A Sequence 35418, A
35	38	47.5	630	_	US-10-953-349-35417	Sequence 35417, A
36	37	46.2	15	6	US-10-490-949-2	Sequence 2, Appli
37	37	46.2	273	-	US-10-953-349-4464	Sequence 4464, Ap
38	37	46.2	305		US-11-293-697-4867	Sequence 4867, Ap
39	37	46.2	330		US-10-505-928-656	Sequence 656, App
40	37	46.2	349	6	US-10-953-349-4463	Sequence 4463, Ap
41	37	46.2	367	6	US-10-953-349-4462	Sequence 4462, Ap
42	37	46.2	395	6	US-10-511-937-2599	Sequence 2599, Ap
43	36	45.0	557	7	US-11-293-697-4833	Sequence 4833, Ap
44	36	45.0	666	7	US-11-293-697-3968	Sequence 3968, Ap
45	35	43.8	246	6	US-10-953-349-29161	Sequence 29161, A
46	35	43.8	329	6	US-10-953-349-29160	Sequence 29160, A
47	35	43.8	349	6	US-10-953-349-948	Sequence 948, App
48	35	43.8	352	6	US-10-953-349-21108	Sequence 21108, A
49	35	43.8	387	6	US-10-953-349-21107	Sequence 21107, A
50	35	43.8	396	6	US-10-953-349-21106	Sequence 21106, A
51	35	43.8	417	6	US-10-953-349-29159	Sequence 29159, A
52	35	43.8	419		US-10-953-349-1054	Sequence 1054, Ap
53	34	42.5	282		US-10-953-349-14698	Sequence 14698, A
54	34	42.5	389		US-11-122-986-185	Sequence 185, App
55	34	42.5	389		US-11-122-986-187	Sequence 187, App
56	33.5	41.9	194		US-10-953-349-7966	Sequence 7966, Ap
57	33.5	41.9	200		US-10-953-349-7965	Sequence 7965, Ap
58 5.0	33	41.2	138		US-10-953-349-20728	Sequence 20728, A
59	33	41.2	148	6	US-10-953-349-8299	Sequence 8299, Ap

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-**12.**rai.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 938-12.rai.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:12:07; Search time 12.7 Seconds

(without alignments)

103.383 Million cell updates/sec

650591

Title:

US-10-001-938-12

Perfect score: 86

Sequence: 1 KKAYRRKALQWHPDK 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched:

650591 segs, 87530628 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Issued Patents AA:*

1: /EMC Celerra_SIDS3/ptodata/2/iaa/5 COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:* 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/iaa/PCTUS COMB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/iaa/RE COMB.pep:*

7: /EMC Celerra SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

ક

Result Query

> No. Score Match Length DB ID

Description

1	86	100.0	277	1	US-08-868-288A-7	Sequence 7, Appli
2	86	100.0	277	2	US-09-235-373-7	Sequence 7, Appli
3	86	100.0	277	2	US-09-388-993-7	Sequence 7, Appli
4	86	100.0	277	2	US-09-501-714-7	Sequence 7, Appli
5	86	100.0	327	2	US-09-949-016-11262	Sequence 11262, A
6	86	100.0	351	1	US-08-868-288A-6	Sequence 6, Appli
7	86	100.0	351	2	US-09-235-373-6	Sequence 6, Appli
8	86	100.0	351	2	US-09-388-993-6	Sequence 6, Appli
9	86	100.0	351	2	US-09-501-714-6	Sequence 6, Appli
10	72	83.7	330	1	US-08-868-288A-3	Sequence 3, Appli
11	72	83.7	330	2	US-09-235-373-3	Sequence 3, Appli
12	72	83.7	330	2	US-09-388-993-3	Sequence 3, Appli
13	72	83.7	330	2	US-09-501-714-3	Sequence 3, Appli
14	70	81.4	411	2	US-10-101-464A-982	Sequence 982, App
15	67	77.9	153	2	US-09-621-976-5129	Sequence 5129, Ap
16	66	76.7	340	1	US-08-974-546-5	Sequence 5, Appli
17	66	76.7	340	2	US-09-949-016-6691	Sequence 6691, Ap
18	66	76.7	363	2	US-09-949-016-8899	Sequence 8899, Ap
19	66	76.7	504	2	US-09-231-529-6	Sequence 6, Appli
20	66	76.7	504	2	US-08-977-816-6	_
	66	76.7	516	2	US-09-949-016-9654	Sequence 6, Appli
21			334	3	US-10-429-223-3	Sequence 9654, Ap
22	65 65	75.6				Sequence 3, Appli
23	65 64	75.6	337	2	US-09-665-479A-8	Sequence 8, Appli
24	64	74.4	86 247	2	US-09-513-999C-6033	Sequence 6033, Ap
25	64	74.4	347	2	US-09-248-796A-19195	Sequence 19195, A
26	64	74.4	348	1	US-08-974-546-1	Sequence 1, Appli
27	64	74.4	397	2	US-09-248-796A-17628	Sequence 17628, A
28	64	74.4	595	2	US-10-104-047-2714	Sequence 2714, Ap
29	63	73.3	87	2	US-09-882-835-4	Sequence 4, Appli
30	63	73.3	102	2	US-09-513-999C-5137	Sequence 5137, Ap
31	63	73.3	118	2	US-09-248-796A-19798	Sequence 19798, A
32	63	73.3	127	2	US-09-370-838-199	Sequence 199, App
33	63	73.3	127	2	US-09-854-133-199	Sequence 199, App
34	63	73.3	397	1	US-08-868-288A-5	Sequence 5, Appli
35	63	73.3	397	2	US-09-235-373-5	Sequence 5, Appli
36	63	73.3	397	2	US-09-388-993-5	Sequence 5, Appli
37	63	73.3	397	2	US-09-919-039-178	Sequence 178, App
38	63	73.3	397	2	US-09-538-092-1052	Sequence 1052, Ap
39	63	73.3	397	2	US-09-501-714-5	Sequence 5, Appli
40	63	73.3	397	3	US-10-429-223-2	Sequence 2, Appli
41	63	73.3	397	3	US-10-429-223-4	Sequence 4, Appli
42	62	72.1	51	1	US-08-346-849-12	Sequence 12, Appl
43	62	72.1	51	1	US-08-293-284A-12	Sequence 12, Appl
44	62	72.1	51	2	US-08-898-300-12	Sequence 12, Appl
45	62	72.1	51	2	US-08-824-513-12	Sequence 12, Appl
46	62	72.1	147	2	US-09-513-999C-6925	Sequence 6925, Ap
47	61	70.9	54	1	US-08-346-849-13	Sequence 13, Appl
48	61	70.9	54	1	US-08-293-284A-13	Sequence 13, Appl
49	61	70.9	54	2	US-08-898-300-13	Sequence 13, Appl
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52	60	69.8	49	1	US-08-346-849-11	Sequence 11, Appl
53	60	69.8	49	1	US-08-293-284A-11	Sequence 11, Appl
54	60	69.8	49	2	US-08-898-300-11	Sequence 11, Appl
55	60	69.8	49	2	US-08-824-513-11	Sequence 11, Appl
56	60	69.8	99	2	US-09-248-796A-19786	Sequence 19786, A
57	60	69.8	138	2	US-09-270-767-42296	Sequence 42296, A
58	60	69.8	358	1	US-08-868-288A-1	Sequence 1, Appli
59	60	69.8	358	2	US-09-235-373-1	Sequence 1, Appli
60	60	69.8	358	2	US-09-388-993-1	Sequence 1, Appli

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938 12.rapbm.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 12.rapbm.

start

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

June 2, 2006, 19:45:16; Search time 63.4 Seconds

(without alignments)

109.593 Million cell updates/sec

Title: US-10-001-938-12

Perfect score: 86

1 KKAYRRKALQWHPDK 15 Sequence:

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

2097797 seqs, 463214858 residues Searched:

2097797 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 1000 summaries

Published Applications AA Main:* Database :

1: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

4: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query No. Score Match Length DB ID Description 86 100.0 15 4 US-10-001-938-12 Sequence 12, Appl

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OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:44:08; Search time 3.1 Seconds

(without alignments)

55.960 Million cell updates/sec

Title:

US-10-001-938-12

Perfect score: 86

1 KKAYRRKALQWHPDK 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

Sequence:

58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seg length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published_Applications AA New:*

/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:*

2: /EMC_Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 NEW PUB.pep:*

4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /EMC Celerra SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10 NEW_PUB.pep:*

7: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /EMC Celerra SIDS3/ptodata/2/pubpaa/US60 NEW PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

કૃ

No.	Score	Match	Length	DB	ID	Description
1	86	100.0	15	6	US-10-490-949-21	Sequence 21, Appl
2	73	84.9	465	6	US-10-953-349-8070	Sequence 8070, Ap
3	73	84.9	473	6	US-10-953-349-8069	Sequence 8069, Ap
4	73	84.9	482	6	US-10-953-349-8068	Sequence 8068, Ap
5	71	82.6	349	6	US-10-953-349-948	Sequence 948, App
6	70	81.4	335	6	US-10-953-349-2182	Sequence 2182, Ap
7	70	81.4	336	6	US-10-953-349-33810	Sequence 33810, A
8	70	81.4	343	6	US-10-953-349-2181	Sequence 2181, Ap
9	70	81.4	430	6	US-10-953-349-33809	Sequence 33809, A
10	66	76.7	15	6	US-10-490-949-22	Sequence 22, Appl
11	66	76.7	504	6	US-10-511-937-2547	Sequence 2547, Ap
12	63	73.3	15	6	US-10-490-949-23	Sequence 23, Appl
13	63	73.3	397	7	US-11-293-697-3837	Sequence 3837, Ap
14	59	68.6	119	6	US-10-953-349-28161	Sequence 28161, A
15	59	68.6	147	6	US-10-953-349-28160	Sequence 28160, A
16	59	68.6	155	6	US-10-953-349-28159	Sequence 28159, A
17	59	68.6	190	6	US-10-953-349-28214	Sequence 28214, A
18	59	68.6	191	6	US-10-953-349-28213	Sequence 28213, A
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20	58	67.4	95	6	US-10-953-349-31080	Sequence 31080, A
21	58	67.4	156		US-10-953-349-5018	Sequence 5018, Ap
22	56	65.1	420		US-10-953-349-13709	Sequence 13709, A
23	55	64.0	15		US-10-490-949-3	Sequence 3, Appli
24	55	64.0	340		US-10-953-349-24393	Sequence 24393, A
25	55	64.0	427	6	US-10-953-349-24392	Sequence 24392, A
26	55	64.0	445	6	US-10-953-349-24391	Sequence 24391, A
27	55	64.0	530		US-10-953-349-20585	Sequence 20585, A
28	54	62.8	199		US-10-953-349-9116	Sequence 9116, Ap
29 30	54 53	62.8 61.6	248		US-10-953-349-9115 US-10-953-349-23847	Sequence 9115, Ap
31	53	61.6	305 317	6	US-10-953-349-23647 US-10-953-349-11729	Sequence 23847, A Sequence 11729, A
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33	53	61.6	419	6	US-10-953-349-1054	Sequence 1057, Ap
34	52	60.5	273		US-10-953-349-4464	Sequence 4464, Ap
35	52	60.5	349	6	US-10-953-349-4463	Sequence 4463, Ap
36	52	60.5	367	6	US-10-953-349-4462	Sequence 4462, Ap
37	51	59.3	391	6	US-10-953-349-7627	Sequence 7627, Ap
38	49	57.0	250		US-10-953-349-22808	Sequence 22808, A
39	49	57.0	389		US-11-122-986-185	Sequence 185, App
40	49	57.0	389		US-11-122-986-187	Sequence 187, App
41	48	55.8	379	6	US-10-953-349-11645	Sequence 11645, A
42	47	54.7	422	6	US-10-953-349-17849	Sequence 17849, A
43	47	54.7	453	6	US-10-953-349-17848	Sequence 17848, A
44	47	54.7	467	6	US-10-953-349-17847	Sequence 17847, A
45	47	54.7	583	6	US-10-953-349-35418	Sequence 35418, A
46	47	54.7	630	6	US-10-953-349-35417	Sequence 35417, A
47	46	53.5	313	6	US-10-953-349-23774	Sequence 23774, A
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55	45	52.3	138		US-10-953-349-39107	Sequence 39107, A
56	45	52.3	174		US-10-953-349-39106	Sequence 39106, A
57 50	45	52.3	338		US-10-953-349-20361	Sequence 20361, A
58 59	45 45	52.3 52.3	385 488	6 6	US-10-953-349-20360 US-10-953-349-20359	Sequence 20360, A Sequence 20359, A
JJ	43	32.3	400	O	05-10-333-343-20333	pedaetice 50000, H

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-13.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-0(13.rai.

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:12:07; Search time 12.7 Seconds

(without alignments)

103.383 Million cell updates/sec

Title: US-10-001-938-13

Perfect score: 82

Sequence: 1 KRAYRRQALRYHPDK 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length I)B	ID	Description	
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2	82	100.0	340	2	US-09-949-016-6691	Sequence 6691, Ap	

3	82	100.0	363	2	US-09-949-016-8899	_	8899, Ap
4	69	84.1	334	3	US-10-429-223-3	•	3, Appli
5	69	84.1	337	2	US-09-665-479A-8	•	8, Appli
6	68	82.9	348	1	US-08-974-546-1	Sequence	1, Appli
7	67	81.7	54	1	US-08-346-849-13	Sequence	13, Appl
8	67	81.7	54	1	US-08-293-284A-13	Sequence	13, Appl
9	67	81.7	54	2	US-08-898-300-13	Sequence	13, Appl
10	67	81.7	54	2	US-08-824-513-13	Sequence	13, Appl
11	67	81.7	347	2	US-09-248-796A-19195	Sequence	19195, A
12	67	81.7	397	2	US-09-248-796A-17628	•	17628, A
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14	66	80.5	102	2	US-09-513-999C-5137	-	5137, Ap
15	66	80.5	127	2	US-09-370-838-199		199, App
16	66	80.5	127	2	US-09-854-133-199	_	199, App
17	66	80.5	277	1	US-08-868-288A-7	-	7, Appli
18	66	80.5	277	2	US-09-235-373-7	_	7, Appli
		80.5	277	2	US-09-388-993-7	_	7, Appli
19	66					-	
20	66	80.5	277	2	US-09-501-714-7	-	7, Appli
21	66	80.5	327	2	US-09-949-016-11262	- .	11262, A
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23	66	80.5	351	2	US-09-235-373-6	_	6, Appli
24	66	80.5	351	2	US-09-388-993-6	Sequence	6, Appli
25	66	80.5	351	2	US-09-501-714-6	_	6, Appli
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33	66	80.5	397	3	US-10-429-223-4	Sequence	4, Appli
34	66	80.5	734	2	US-09-248-796A-16776	Sequence	16776, A
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OM protein - protein search, using sw model

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(without alignments)

109.593 Million cell updates/sec

Title: US-10-001-938-13

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Listing first 1000 summaries

Published Applications AA Main:* Database :

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SUMMARIES

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55.960 Million cell updates/sec

Title:

US-10-001-938-13

Perfect score: 82

1 KRAYRRQALRYHPDK 15

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Searched:

Sequence:

58871 seqs, 11565156 residues

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database :

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1 82 100.0 15 6 US-10-490-949-22 Sequence 22, Appl 2 66 80.5 15 6 US-10-490-949-21 Sequence 21, Appl 3 66 80.5 337 7 US-11-293-697-3817 Sequence 3337, Appl 4 66 80.5 337 7 US-11-293-697-3817 Sequence 33810, A 5 62 75.6 336 6 US-10-953-349-33810 Sequence 33810, A 6 62 75.6 430 6 US-10-953-349-33809 Sequence 33810, A 7 61 74.4 349 6 US-10-953-349-3180 Sequence 33809, A 7 61 74.4 349 6 US-10-953-349-9116 Sequence 918, Appl 8 59 72.0 199 6 US-10-953-349-9116 Sequence 9116, Ap 9 59 72.0 343 6 US-10-953-349-9115 Sequence 2182, Ap 11 59 72.0 343 6 US-10-953-349-2182 Sequence 2182, Ap 12 58 70.7 15 6 US-10-953-349-2181 Sequence 2182, Ap 12 58 70.7 15 6 US-10-953-349-2181 Sequence 2182, Ap 12 58 70.7 15 6 US-10-953-349-2181 Sequence 2182, Ap 12 58 70.7 530 6 US-10-953-349-2181 Sequence 315, Appl 13 58 70.7 530 6 US-10-953-349-2010 Sequence 3170, Ap 15 56 68.3 340 US-10-953-349-8069 Sequence 3187, Ap 16 US-10-953-349-8069 Sequence 8070, Ap 17 57 69.5 465 6 US-10-953-349-8069 Sequence 8070, Ap 17 57 69.5 465 6 US-10-953-349-8069 Sequence 8066, Ap 18 56 68.3 340 6 US-10-953-349-3161 Sequence 23847, A 19 56 68.3 340 6 US-10-953-349-2181 Sequence 23847, A 19 56 68.3 420 6 US-10-953-349-2181 Sequence 23847, A 20 54 65.9 119 6 US-10-953-349-2181 Sequence 23847, A 20 54 65.9 190 6 US-10-953-349-2181 Sequence 23814, A 20 54 0S-10-953-349-2181 Sequence 23	No.	Score	Match	Length	DB	ID	Description
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					_		-
59 45 54.9 422 6 US-10-953-349-17849 Sequence 17849, A							-
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SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-14.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 14.rai.

start

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

June 2, 2006, 19:08:52; Search time 11.4238 Seconds Run on:

(without alignments)

114.932 Million cell updates/sec

Title: US-10-001-938-14

Perfect score: 81

Sequence: 1 KKAYRKLALKYHPDK 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

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6: /EMC Celerra SIDS3/ptodata/2/iaa/RE_COMB.pep:* /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	81	100.0	127	2	US-09-854-133-199	Sequence	199, App
5	81	100.0	397	1	US-08-868-288A-5	•	5, Appli
6	81	100.0	397	2	US-09-235-373-5	_	5, Appli
7	81	100.0	397	2	US-09-388-993-5	-	5, Appli
8	81	100.0	397	2	US-09-919-039-178		178, App
9	81	100.0	397	2	US-09-538-092-1052	-	1052, Ap
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13	79 70	97.5	348	_		•	1, Appli
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15	78	96.3	406	2	US-09-438-185A-34		34, Appl
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18	77	95.1	52	2	US-08-898-300-10	•	10, Appl
19	77	95.1	52	2	US-08-824-513-10	•	10, Appl
20	77	95.1	147	2	US-09-513-999C-6925	•	6925, Ap
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24	76	93.8	51	2	US-08-824-513-12	Sequence	12, Appl
25	76	93.8	330	1	US-08-868-288A-3	Sequence	3, Appli
26	76	93.8	330	2	US-09-235-373-3	-	3, Appli
27	76	93.8	330	2	US-09-388-993-3	-	3, Appli
28	76	93.8	330	2	US-09-501-714-3	-	3, Appli
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63	67	82.7	206	2	US-09-830-230A-294	•	294, App
0.5	0 /	92.1	200	_	22 33 330 230n 234	204401100	, · PP

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938 14.rapbm.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 14.rapbm.

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OM protein - protein search, using sw model

June 2, 2006, 19:29:53; Search time 75.9934 Seconds Run on:

(without alignments)

91.432 Million cell updates/sec

Title: US-10-001-938-14

Perfect score: 81

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Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

2097797 seqs, 463214858 residues Searched:

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 1000 summaries

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2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

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5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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40	77	95.1	132	3	US-09-764-868-1163		Sequence	1163, Ap
41	77	95.1	220	5	US-10-494-921-52		Sequence	52, Appl
42	77	95.1	223	6	US-11-097-143-41196		Sequence	41196, A
43	77	95.1	249	6	US-11-097-143-24078		-	24078, A
			276				4	•
44	77	95.1		4	US-10-220-120-320		_	320, App
45	77	95.1	297	3	US-09-764-868-1162		-	1162, Ap
46	77	95.1	373	3	US-09-764-868-789		Sequence	789, App
47	77	95.1	379	5	US-10-489-695-9		Sequence	9, Appli
48	77	95.1	397	3	US-09-989-890-262		-	262, App
			51	4	US-10-390-472-12		-	12, Appl
49	76	93.8					-	
50	76	93.8	60	3	US-09-764-868-790		-	790, App
51	76	93.8	60	3	US-09-764-891-3746		Sequence	3746, Ap
52	76	93.8	112	4	US-10-767-701-39994		Sequence	39994, A
53	76	93.8	143	4	US-10-424-599-230584		-	230584,
54	76	93.8	158	4	US-10-425-114-48912		-	48912, A
							•	·
55	76	93.8	196	5	US-10-450-763-58941		•	58941, A
56	76	93.8	242	4	US-10-264-049-2674		•	2674, Ap
57	76	93.8	255	4	US-10-437-963-123368		Sequence	123368,
58	76	93.8	276	4	US-10-282-122A-47226	-	Sequence	47226, A
59	76	93.8	326	4	US-10-425-115-300448		Sequence	
				_			_	
60	76	93.8	369	4	US-10-369-493-19646		•	19646, A
61	76	93.8	407	4	US-10-425-115-303598		Sequence	
62	76	93.8	413	4	US-10-425-114-56774		Sequence	56774, A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-14.rapbn.

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Comments / **Suggestions**

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-001-938-14.rapbn.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:30:30; Search time 3.57616 Seconds

(without alignments)

48.509 Million cell updates/sec

Title: US-10-001-938-14

Perfect score: 81

1 KKAYRKLALKYHPDK 15 Sequence:

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Published Applications AA New:* Database :

/EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US07 NEW PUB.pep:*

4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 NEW PUB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT NEW PUB.pep:* 6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10 NEW PUB.pep:*

7: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11 NEW PUB.pep:*

/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

&

Result

No.	Score	Match	Length	DB	ID	Description
1	81	100.0	15	6	US-10-490-949-23	Sequence 23, Appl
2	81	100.0	397	7	US-11-293-697-3837	Sequence 3837, Ap
3	74	91.4	335	6	US-10-953-349-2182	Sequence 2182, Ap
4	74	91.4	343	6	US-10-953-349-2181	Sequence 2181, Ap
5	72	88.9	426	7	US-11-293-697-4751	Sequence 4751, Ap
6	71	87.7	305	6	US-10-953-349-23847	Sequence 23847, A
7	71	87.7	336	6	US-10-953-349-33810	Sequence 33810, A
8	71	87.7	430	6	US-10-953-349-33809	Sequence 33809, A
9	69	85.2	465	6	US-10-953-349-8070	Sequence 8070, Ap
10	69	85.2	473	6	US-10-953-349-8069	Sequence 8069, Ap
11	69	85.2	482	6	US-10-953-349-8068	Sequence 8068, Ap
12	67	82.7	15	6	US-10-490-949-3	Sequence 3, Appli
13	67	82.7	273	6	US-10-953-349-4464	Sequence 4464, Ap
14	67	82.7	349	6	US-10-953-349-4463	Sequence 4463, Ap
15	67	82.7	367	6	US-10-953-349-4462	Sequence 4462, Ap
16	67	82.7	389	7	US-11-122-986-185	Sequence 185, App
17	67	82.7	389	7	US-11-122-986-187	Sequence 187, App
18	66	81.5	15	6	US-10-490-949-22	Sequence 22, Appl
19	66 66	81.5	199	6	US-10-953-349-9116	Sequence 9116, Ap
20	66 66	81.5	248	6 6	US-10-953-349-9115	Sequence 9115, Ap
21 22	66 65	81.5 80.2	349 420	6	US-10-953-349-948 US-10-953-349-13709	Sequence 948, App Sequence 13709, A
23	65	80.2	583	6	US-10-953-349-15709 US-10-953-349-35418	Sequence 35418, A
24	65	80.2	630	6	US-10-953-349-35417	Sequence 35417, A
25	63	77.8	15	6	US-10-490-949-21	Sequence 21, Appl
26	62	76.5	95	6	US-10-953-349-31080	Sequence 31080, A
27	62	76.5	156	6	US-10-953-349-5018	Sequence 5018, Ap
28	62	76.5	417	6	US-10-953-349-16377	Sequence 16377, A
29	62	76.5	419	6	US-10-953-349-1054	Sequence 1054, Ap
30	62	76.5	504	6	US-10-511-937-2547	Sequence 2547, Ap
31	61	75.3	313	6	US-10-953-349-23774	Sequence 23774, A
32	61	75.3	334	6	US-10-953-349-23773	Sequence 23773, A
33	60	74.1	380	6	US-10-953-349-7175	Sequence 7175, Ap
34	60	74.1	391	6	US-10-953-349-7174	Sequence 7174, Ap
35	60	74.1	442	6	US-10-953-349-7173	Sequence 7173, Ap
36	59	72.8	250	6	US-10-953-349-22808	Sequence 22808, A
37	59	72.8	530	6	US-10-953-349-20585	Sequence 20585, A
38	58	71.6	110	6	US-10-953-349-54	Sequence 54, Appl
39	58	71.6	124	6	US-10-953-349-53	Sequence 53, Appl
40	58	71.6	162	6	US-10-953-349-52	Sequence 52, Appl
41	57	70.4	189	7	US-11-293-697-4556	Sequence 4556, Ap
42	56	69.1	333	6	US-10-953-349-2863	Sequence 2863, Ap
43	56	69.1	333	6	US-10-953-349-11247	Sequence 11247, A
44	54	66.7	190	6	US-10-953-349-28214	Sequence 28214, A
45	54	66.7	191	6	US-10-953-349-28213	Sequence 28213, A
46	53	65.4	340	6	US-10-953-349-24393	Sequence 24393, A
47	53	65.4	427	6	US-10-953-349-24392	Sequence 24392, A
48	53	65.4	445	6	US-10-953-349-24391	Sequence 24391, A
49 50	52 52	64.2 64.2	157 192	6 6	US-10-953-349-38105	Sequence 38105, A
51	51	63.0	422	6	US-10-953-349-38104 US-10-953-349-17849	Sequence 38104, A Sequence 17849, A
52	51	63.0	453	6	US-10-953-349-17848	Sequence 17848, A
53	51	63.0	467	6	US-10-953-349-17847	Sequence 17847, A
54	49	60.5	605	6	US-10-953-349-2076	Sequence 2076, Ap
55	49	60.5	619	6	US-10-953-349-2075	Sequence 2075, Ap
56	49	60.5	630	6	US-10-953-349-2074	Sequence 2074, Ap
57	48	59.3	119	6	US-10-953-349-28161	Sequence 28161, A
58	48	59.3	138	6	US-10-953-349-39107	Sequence 39107, A
59	48	59.3	147	6	US-10-953-349-28160	Sequence 28160, A
						•

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-15

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 15.rai.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

June 2, 2006, 19:08:52; Search time 11.4238 Seconds Run on:

(without alignments)

114.932 Million cell updates/sec

Title: US-10-001-938-15

Perfect score: 73

Sequence: 1 FRSVSTSTTFVQGRR 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

> 1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:* 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:* 3: /EMC Celerra_SIDS3/ptodata/2/iaa/7 COMB.pep:* 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:* 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:* 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:* /EMC Celerra SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description		
1 2	73 73	100.0	_		US-08-868-288A-7 US-09-235-373-7	Sequence 7, Appli Sequence 7, Appli		

2	7.0	100 0	077	2	HG 00 300 002 7	9	7 7 2 2 2 3
3	73	100.0	277	2	US-09-388-993-7	Sequence 7	
4	73	100.0	277	2	US-09-501-714-7	Sequence 7	
5	73	100.0	327	2	US-09-949-016-11262	Sequence 1	
6	73	100.0	351	1	US-08-868-288A-6	Sequence 6	
7	73	100.0	351	2	US-09-235-373-6	Sequence 6	- -
8	73	100.0	351	2	US-09-388-993-6	Sequence 6	6, Appli
9	73	100.0	351	2	US-09-501-714-6	Sequence 6	6, Appli
10	49	67.1	330	1	US-08-868-288A-3	Sequence 3	3, Appli
11	49	67.1	330	2	US-09-235-373-3	Sequence 3	3, Appli
12	49	67.1	330	2	US-09-388-993-3	Sequence 3	3, Appli
13	49	67.1	330	2	US-09-501-714-3	Sequence 3	
14	40	54.8	83	2	US-09-107-433-4269	Sequence 4	
15	40	54.8	108	2	US-09-107-433-5049	Sequence 5	_
16	38	52.1	269	2	US-09-252-991A-24237	Sequence 2	· -
17	38	52.1	339	2	US-10-104-047-2843	Sequence 2	
				2	US-10-104-047-2843	•	
18	38	52.1	540	_		Sequence 3	•
19	37	50.7	165	2	US-09-270-767-37910	Sequence 3	
20	37	50.7	165	2	US-09-270-767-53127	Sequence 5	
21	37	50.7	464	2	US-09-693-746-14	Sequence 1	• •
22	37	50.7	1271	1	US-08-095-734-2	Sequence 2	
23	37	50.7	1271	1	US-08-444-623-2	Sequence 2	2, Appli
24	37	50.7	1271	2	US-08-471-869-2	Sequence 2	2, Appli
25	37	50.7	1271	2	US-09-342-563-2	Sequence 2	2, Appli
26	37	50.7	1271	5	PCT-US94-08267-2	Sequence 2	2, Appli
27	36	49.3	102	2	US-09-471-276-1004	Sequence 1	1004, Ap
28	36	49.3	103	2	US-09-673-395A-348	Sequence 3	· · · · · · · · · · · · · · · · · · ·
29	36	49.3	108	2	US-09-107-433-5048	Sequence 5	
30	36	49.3	108	2	US-09-107-433-5050	Sequence 5	· -
31	36	49.3	476	2	US-09-902-540-14917	Sequence 1	•
32	36	49.3	788	1	US-08-194-338-12	Sequence 1	-
33	36	49.3	859	1	US-08-053-614-2	Sequence 2	
34	36	49.3	859	1	US-08-316-397B-2	•	
				_		Sequence 2	
35	36	49.3	859	1	US-09-034-306-2	Sequence 2	
36	36	49.3	859	2	US-09-259-437-2	Sequence 2	
37	36	49.3	859	5	PCT-US93-09782-2	Sequence 2	
38	36	49.3	1041	2	US-09-999-833A-498	Sequence 4	
39	36	49.3	1041	2	US-09-954-987B-184	Sequence 1	
40	36	49.3	1041	2	US-09-954-987B-186	Sequence 1	·
41	36	49.3	1041	2	US-10-020-445A-498	Sequence 4	498, App
42	36	49.3	1041	2	US-09-978-189-498	Sequence 4	498, App
43	36	49.3	1041	2	US-10-017-085A-498	Sequence 4	498, App
44	36	49.3	1041	3	US-10-145-129A-498	Sequence 4	498, App
45	36	49.3	1041	3	US-10-013-929A-498	Sequence 4	498, App
46	36	49.3	1041	3	US-10-013-917A-498	Sequence 4	498, App
47	36	49.3	1059	2	US-09-954-987B-187	Sequence 1	
48	36	49.3	1181	1	US-08-053-614-4	Sequence 4	
49	36	49.3	1181	1	US-08-316-397B-4	Sequence 4	
50	36	49.3	1181	1	US-09-034-306-4	Sequence 4	. ·
51	36	49.3	1181	2	US-09-259-437-4	Sequence 4	
52	36	49.3	1181	5	PCT-US93-09782-4	Sequence 4	– –
53	35	47.9	80	2	US-09-248-796A-25415	Sequence 2	
5 4	35	47.9	187	2	US-09-248-796A-19489	Sequence 1	•
55	35	47.9	218	2	US-09-489-039A-13787	Sequence :	
						-	·
56	35	47.9	404	2	US-09-242-859A-11	Sequence 1	• • •
57	35	47.9	405	2	US-09-538-092-1059	Sequence	•
58	35	47.9	416	2	US-09-949-016-7485	Sequence	•
59	35	47.9	448	2	US-09-902-540-16109	Sequence 3	<u>-</u>
60	35	47.9	765	2	US-09-543-681A-4287	Sequence 4	-
61	35	47.9	792	2	US-09-248-796A-18842	Sequence :	•
62	35	47.9	824	2	US-10-055-364-43	Sequence 4	
63	35	47.9	874	2	US-08-804-439A-16	Sequence :	16, Appl

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-15.r

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 15.rapbm.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

June 2, 2006, 19:29:53; Search time 75.9934 Seconds Run on:

(without alignments)

91.432 Million cell updates/sec

Title: US-10-001-938-15

Perfect score: 73

Sequence: 1 FRSVSTSTTFVQGRR 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

2097797 segs, 463214858 residues Searched:

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Published_Applications AA Main:* Database :

/EMC Celerra SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:* /EMC Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length :	DB	ID Description				
1	73	100.0	15	4	US-10-001-938-15	Sequence 15, Appl			
2	49	67.1	242	4	US-10-264-049-2674	Sequence 2674, Ap			
3	44	60.3	92	5	US-10-450-763-58559	Sequence 58559, A			

4	44	60.3	164	4	US-10-363-829-341	Sequence	341, App
5	44	60.3	227	4	US-10-220-120-322	Sequence	322, App
6	43	58.9	85	4	US-10-425-115-242949	Sequence	
7	43	58.9	97	4	US-10-425-115-246113	Sequence	
8	42	57.5	1473	4	US-10-437-963-111000	Sequence	
9	41	56.2	52	4	US-10-425-115-210546	Sequence	
10	41	56.2	326	6	US-11-096-568A-7817	•	7817, Ap
11	41	56.2	328	6	US-11-096-568A-7816	•	7816, Ap
12	40	54.8	83	5	US-10-617-320-4269	Sequence	•
13	40	54.8		5	US-10-617-320-4269	-	_
			108	-		•	5049, Ap
14	40	54.8	843	4	US-10-156-761-13999	•	13999, A
15	40	54.8	843	5	US-10-732-923-1579	-	1579, Ap
16	39	53.4	80	4	US-10-424-599-273144	Sequence	
17	39	53.4	123	4	US-10-437-963-122175	Sequence	•
18	39	53.4	509	4	US-10-074-978A-204	Sequence	204, App
19	39	53.4	509	4	US-10-074-978A-205	Sequence	205, App
20	39	53.4	509	4	US-10-074-978A-206	Sequence	206, App
21	39	53.4	513	5	US-10-732-923-1992	Sequence	1992, Ap
22	39	53.4	529	4	US-10-437-963-125175	Sequence	125175,
23	39	53.4	591	5	US-10-450-763-48382	Sequence	48382, A
24	38	52.1	325	4	US-10-282-122A-45976	•	45976, A
25	38	52.1	339	4	US-10-104-047-2843	-	2843, Ap
26	38	52.1	339	6	US-11-072-512-2843		2843, Ap
27	38	52.1	396	3	US-09-925-301-852	•	852, App
28	38	52.1	432	4	US-10-264-049-2915	-	2915, Ap
				_		-	_
29	38	52.1	540	4	US-10-104-047-3747	-	3747, Ap
30	38	52.1	540	6	US-11-072-512-3747	-	3747, Ap
31	38	52.1	582	5	US-10-635-407-16	-	16, Appl
32	38	52.1	622	5	US-10-635-407-138	-	138, App
33	38	52.1	623	4	US-10-116-275-144		144, App
34	38	52.1	623	5	US-10-753-267-10	-	10, Appl
35	38	52.1	623	5	US-10-756-149-5040	_	5040, Ap
36	38	52.1	623	5	US-10-635-407-8	_	8, Appli
37	38	52.1	623	5	US-10-635-407-112	Sequence	112, App
38	38	52.1	623	5	US-10-635-407-114	Sequence	114, App
39	38	52.1	623	5	US-10-635-407-116	Sequence	116, App
40	38	52.1	623	5	US-10-635-407-118	Sequence	118, App
41	38	52.1	623	5	US-10-635-407-120	Sequence	120, App
42	38	52.1	623	5	US-10-635-407-122	Sequence	
43	38	52.1	623	5	US-10-635-407-124	Sequence	• •
44	38	52.1	623	5	US-10-635-407-126	Sequence	
45	38	52.1	623	5	US-10-635-407-128	Sequence	• •
46	38	52.1	623	5	US-10-635-407-130	Sequence	
47	38	52.1	623	5	US-10-635-407-132	Sequence	
48	38	52.1	623	5	US-10-635-407-134	-	134, App
				_	US-10-635-407-134		
49	38	52.1	623	5			136, App
50	38	52.1	623	5	US-10-635-407-140	<u> </u>	140, App
51	38	52.1	623	5	US-10-635-407-142	Sequence	
52	38	52.1	623	5	US-10-635-407-144	-	144, App
53	38	52.1	623	5	US-10-635-407-146	_	146, App
54	38	52.1	623	5	US-10-635-407-148	_	148, App
55	38	52.1	623	5	US-10-635-407-150	_	150, App
56	38	52.1	623	5	US-10-635-407-152	-	152, App
57	38	52.1	623	5	US-10-635-407-154	•	154, App
58	38	52.1	623	5	US-10-878-556A-62	Sequence	62, Appl
59	38	52.1	627	5	US-10-635-407-12	Sequence	12, Appl
60	38	52.1	627	5	US-10-635-407-14	Sequence	14, Appl
61	38	52.1	628	5	US-10-635-407-10	-	10, Appl
62	37	50.7	58	4	US-10-291-265-317		317, App
63	37	50.7	58	6	US-11-000-463-317	-	317, App
64	37	50.7	70	4	US-10-425-115-234142	•	234142,
_	- ,	_ • • •	. •	•		4	

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-15.rapbn.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:30:30; Search time 3.57616 Seconds

(without alignments)

48.509 Million cell updates/sec

Title: US-10-001-938-15

Perfect score: 73

1 FRSVSTSTTFVQGRR 15 Sequence:

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

58871 seqs, 11565156 residues Searched:

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA New: *

/EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:*

/EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 NEW PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /EMC_Celerra SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC_Celerra SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:* /EMC Celerra SIDS3/ptodata/2/pubpaa/US11 NEW PUB.pep:*

/EMC_Celerra SIDS3/ptodata/2/pubpaa/US60 NEW PUB.pep:* 8:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

No.	Score	Match	Length	DB	ID	Description
1	73	100.0	15	6	US-10-490-949-24	Sequence 24, Appl
2	37	50.7	150	6	US-10-953-349-38479	Sequence 38479, A
3	36	49.3	164	6	US-10-953-349-36632	Sequence 36632, A
4	36	49.3	312	6	US-10-953-349-20709	Sequence 20709, A
5	36	49.3	413	6	US-10-953-349-7374	Sequence 7374, Ap
6	36	49.3	445	6	US-10-953-349-7373	Sequence 7373, Ap
7	36	49.3	483	6	US-10-953-349-7372	Sequence 7372, Ap
8	34	46.6	136	7	US-11-293-697-4484	Sequence 4484, Ap
9	34	46.6	272	7	US-11-293-697-4608	Sequence 4608, Ap
10	34	46.6	325	6	US-10-953-349-8881	Sequence 8881, Ap
11	34	46.6	331	6	US-10-953-349-8880	Sequence 8880, Ap
12	34	46.6	342	6	US-10-953-349-8879	Sequence 8879, Ap
13	34	46.6	838	7	US-11-295-336-2	Sequence 2, Appli
14	33	45.2	126	6	US-10-953-349-17379	Sequence 17379, A
15	33	45.2	126	6	US-10-953-349-23925	Sequence 23925, A
16	33	45.2	134	6	US-10-953-349-17378	Sequence 17378, A
17	33	45.2	134	6	US-10-953-349-23924	Sequence 23924, A
18	33	45.2	134	6	US-10-953-349-26245	Sequence 26245, A
19	33	45.2	137	6	US-10-953-349-28995	Sequence 28995, A
20	33	45.2	160	6	US-10-953-349-17377	Sequence 17377, A
21	33	45.2	160	6	US-10-953-349-23923	Sequence 23923, A
22	33	45.2	195	6	US-10-953-349-31424	Sequence 31424, A
23	33	45.2	197	6	US-10-953-349-15564	Sequence 15564, A
24	33	45.2	200	6	US-10-953-349-10713	Sequence 10713, A
25	33	45.2	211	6	US-10-953-349-31423	Sequence 31423, A
26	33	45.2	236	6	US-10-953-349-31422	Sequence 31422, A
27	33	45.2	4373	7	US-11-118-524-2	Sequence 2, Appli
28	32	43.8	159	7	US-11-122-986-221	Sequence 221, App
29	32	43.8	159	7	US-11-122-986-223	Sequence 223, App
30	32	43.8	211	6	US-10-953-349-4200	Sequence 4200, Ap
31 32	32 32	43.8 43.8	215 246	7 6	US-11-249-111-95 US-10-953-349-4199	Sequence 95, Appl
33	32	43.8	255	6	US-10-953-349-4199 US-10-953-349-7139	Sequence 4199, Ap Sequence 7139, Ap
34	32	43.8	258	6	US-10-953-349-7139	Sequence 7139, Ap
35	32	43.8	272	6	US-10-953-349-4198	Sequence 4198, Ap
36	32	43.8	272	6	US-10-953-349-13203	Sequence 13203, A
37	32	43.8	288	6	US-10-953-349-13202	Sequence 13203, A
38	32	43.8	310	6	US-10-953-349-13201	Sequence 13201, A
39	32	43.8	314	6	US-10-953-349-28317	Sequence 28317, A
40	32	43.8	371	6	US-10-953-349-28316	Sequence 28316, A
41	32	43.8	433	6	US-10-953-349-7137	Sequence 7137, Ap
42	32	43.8	632	6	US-10-953-349-12946	Sequence 12946, A
43	32	43.8	635	6	US-10-953-349-12945	Sequence 12945, A
44	32	43.8	644	6	US-10-953-349-12944	Sequence 12944, A
45	32	43.8	1033	7	US-11-121-154-207	Sequence 207, App
46	31	42.5	109	7	US-11-254-679-9	Sequence 9, Appli
47	31	42.5	122	6	US-10-953-349-20387	Sequence 20387, A
48	31	42.5	148	6	US-10-953-349-20385	Sequence 20385, A
49	31	42.5	162	6	US-10-953-349-30554	Sequence 30554, A
50	31	42.5	175	6	US-10-953-349-33661	Sequence 33661, A
51	31	42.5	177	6	US-10-953-349-16399	Sequence 16399, A
52	31	42.5	179	6	US-10-953-349-30553	Sequence 30553, A
53	31	42.5	184	6	US-10-953-349-16398	Sequence 16398, A
54	31	42.5	184	6	US-10-953-349-33660	Sequence 33660, A
55	31	42.5	203	6	US-10-953-349-30552	Sequence 30552, A
56	31	42.5	217	6	US-10-953-349-23578	Sequence 23578, A
57	31	42.5	218	6	US-10-953-349-23577	Sequence 23577, A
58 50	31	42.5	256	6	US-10-953-349-23576	Sequence 23576, A
59	31	42.5	256	6	US-10-953-349-39697	Sequence 39697, A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-16.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 16.rai.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2006, 19:08:52; Search time 11.4238 Seconds

(without alignments)

114.932 Million cell updates/sec

Title: US-10-001-938-16

Perfect score: 82

1 PGMVQQIQSVCMECQ 15 Sequence:

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

650591 seqs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Issued Patents AA:* Database :

> 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/iaa/PCTUS COMB.pep:* 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:* /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length DB ID			Description
1	82	100.0	397	1	US-08-868-288A-5	Sequence 5, Appli
2	82	100.0	397	2	US-09-235-373-5	Sequence 5, Appli

3	82	100.0	397	2	US-09-388-993-5	Sequence	5, Appli
4	82	100.0	397	2	US-09-919-039-178	Sequence	178, App
5	82	100.0	397	2	US-09-538-092-1052	Sequence	1052, Ap
6	82	100.0	397	2	US-09-501-714-5	•	5, Appli
7	71	86.6	239	2	US-10-104-047-2162		2162, Ap
8	71	86.6	397	3	US-10-429-223-2	-	
				_		•	2, Appli
9	71	86.6	397	3	US-10-429-223-4	_	4, Appli
10	51	62.2	419	1	US-08-686-417-3	-	3, Appli
11	50	61.0	330	2	US-09-248-796A-19977	Sequence	19977, A
12	49	59.8	459	1	US-08-870-518-4	Sequence	4, Appli
13	45	54.9	397	2	US-09-248-796A-17628	•	17628, A
14	45	54.9	486	1	US-08-870-518-3	•	3, Appli
15	44	53.7	345	2	US-09-248-796A-14816	-	14816, A
				_			
16	42	51.2	492	2	US-09-107-532A-6385	•	6385, Ap
17	40	48.8	273	2	US-09-248-796A-17627		17627, A
18	39	47.6	114	2	US-09-865-483-8	Sequence	8, Appli
19	39	47.6	114	2	US-10-726-555-8	Sequence	8, Appli
20	39	47.6	116	2	US-08-397-411-4	Sequence	4, Appli
21	39	47.6	119	1	US-07-634-278-60	Sequence	60, Appl
22	39	47.6	119	1	US-08-477-728-60	Sequence	
23	39	47.6	119	1	US-08-474-040-60	Sequence	• • •
				_		•	
24	39	47.6	119	1	US-08-487-200-60	_	60, Appl
25	39	47.6	119	2	US-08-484-537-60	Sequence	60, Appl
26	39	47.6	119	3	US-09-718-998-60	Sequence	60, Appl
27	39	47.6	124	2	US-09-270-767-48315	Sequence	48315, A
28	39	47.6	138	1	US-07-634-278-33	Sequence	33, Appl
29	39	47.6	138	1	US-08-477-728-33	Sequence	
30	39	47.6	138	1	US-08-474-040-33	-	33, Appl
				_		_	
31	39	47.6	138	1	US-08-487-200-33	-	33, Appl
32	39	47.6	138	2	US-08-484-537-33		33, Appl
33	39	47.6	138	3	US-09-718-998-33	-	33, Appl
34	39	47.6	234	2	US-09-040-483-5	Sequence	5, Appli
35	39	47.6	234	2	US-08-740-036-5	Sequence	5, Appli
36	39	47.6	234	3	US-09-645-399-5	Sequence	5, Appli
37	39	47.6	282	2	US-10-104-047-2824	-	2824, Ap
38	39	47.6	470	2	US-10-104-047-3177	•	3177, Ap
39	39	47.6	478	2	US-09-770-916-2	-	2, Appli
				_		•	
40	39	47.6	582	1	US-08-989-386-1	-	1, Appli
41	39	47.6	588	2	US-10-094-749-2309	-	2309, Ap
42	38.5	47.0	362	2	US-09-252-991A-18068	-	18068, A
43	38.5	47.0	1752	2	US-09-949-002-294	Sequence	294, App
44	38.5	47.0	1917	2	US-09-949-002-485	Sequence	485, App
45	38	46.3	85	2	US-09-263-933-6	Sequence	6, Appli
46	38	46.3	85	2	US-09-263-933-13	_	13, Appl
47	38	46.3	85	2	US-09-263-933-20		20, Appl
48	38	46.3	85	2	US-09-919-901-6	•	_ ·
						-	6, Appli
49	38	46.3	85	2	US-09-919-901-13	_	13, Appl
50	38	46.3	85	2	US-09-919-901-20	_	20, Appl
51	38	46.3	85	2	US-10-191-966-6	Sequence	6, Appli
52	38	46.3	85	2	US-10-191-966-13	Sequence	13, Appl
53	38	46.3	85	2	US-10-191-966-20	Sequence	20, Appl
54	38	46.3	228	2	US-10-104-047-2483	-	2483, Ap
55	38	46.3	243	2	US-09-469-242-2		2, Appli
56	38	46.3	328	2	US-09-350-702-16	_	16, Appl
				2	US-09-538-092-1165	-	
57	38	46.3	680			•	1165, Ap
58	38	46.3	680	2	US-09-949-016-6637	-	6637, Ap
59	38	46.3	708	2	US-09-949-016-6638	•	6638, Ap
60	38	46.3	712	2	US-09-949-016-7340	•	7340, Ap
61	. 38	46.3	712	2	US-09-949-016-7341	Sequence	7341, Ap
62	38	46.3	2307	2	US-09-263-933-2	Sequence	2, Appli
63	38	46.3	2307	2	US-09-263-933-9	•	9, Appli
		+ -				1	- 1

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938 16.rapbm.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

June 2, 2006, 19:29:53; Search time 75.9934 Seconds Run on:

(without alignments)

91.432 Million cell updates/sec

US-10-001-938-16 Title:

Perfect score: 82

1 PGMVQQIQSVCMECQ 15 Sequence:

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

2097797 seqs, 463214858 residues Searched:

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 1000 summaries

Published Applications AA Main:* Database :

> 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

> 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10A PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:* 6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11 PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ક Result Query No. Score Match Length DB ID Description 82 100.0 15 4 US-10-001-938-16 Sequence 16, Appl 1

_							
2	82	100.0	165	4	US-10-106-698-6762	Sequence	6762, Ap
3	82	100.0	165	5	US-10-473-127-1142	Sequence	1142, Ap
4	82	100.0	252	4	US-10-264-049-4191	Sequence	4191, Ap
5	82	100.0	258	5	US-10-473-127-1141	Sequence	1141, Ap
6	82	100.0	258	5	US-10-473-127-1146	Sequence	1146, Ap
7	82	100.0	397	3	US-09-919-039-178	Sequence	178, App
8	82	100.0	397	5	US-10-473-127-1138	Sequence	1138, Ap
9	82	100.0	397	5	US-10-473-127-1139	•	1139, Ap
10	82	100.0	397	5	US-10-473-127-1140	Sequence	_
11	82	100.0	397	5	US-10-473-127-1143	Sequence	_
12	82	100.0	397	5	US-10-473-127-1144	•	1144, Ap
13	82	100.0	397	5	US-10-473-127-1145	•	1145, Ap
14		100.0	397	5		_	-
	82				US-10-756-149-4727	-	4727, Ap
15	82	100.0	397	5	US-10-631-467-559	_	559, App
16	82	100.0	397	5	US-10-631-467-1386	•	1386, Ap
17	82	100.0	397	5	US-10-878-556A-155	_	155, App
18	82	100.0	408	5	US-10-450-763-40099	•	40099, A
19	72	87.8	291	5	US-10-450-763-40097	Sequence	40097, A
20	71	86.6	239	4	US-10-104-047-2162	Sequence	2162, Ap
21	71	86.6	239	6	US-11-072-512-2162	Sequence	2162, Ap
22	71	86.6	397	4	US-10-108-260A-3837	Sequence	3837, Ap
23	71	86.6	397	4	US-10-429-223-2	Sequence	2, Appli
24	71	86.6	397	4	US-10-429-223-4		4, Appli
25	71	86.6	426	4	US-10-108-260A-4751	-	4751, Ap
26	65	79.3	412	5	US-10-965-898-18	-	18, Appl
27	65	79.3	479	4	US-10-788-792-186	-	186, App
28	59	72.0	244	4	US-10-425-115-217751	Sequence	
29	59	72.0	420	4	US-10-767-701-46164	•	46164, A
				_		•	·
30	57	69.5	363	4	US-10-425-115-304214	Sequence	· · · · · · · · · · · · · · · · · · ·
31	56	68.3	211	4	US-10-767-701-47401	•	47401, A
32	56	68.3	330	6	US-11-096-568A-16062	•	16062, A
33	56	68.3	336	6	US-11-096-568A-16061	-	16061, A
34	56	68.3	370	4	US-10-259-194A-44	-	44, Appl
35	56	68.3	417	4	US-10-437-963-194306	Sequence	
36	56	68.3	417	4	US-10-425-115-307680	Sequence	307680,
37	56	68.3	418	4	US-10-425-115-307678	Sequence	307678,
38	56	68.3	418	4	US-10-425-115-307679	Sequence	307679,
39	56	68.3	433	4	US-10-425-114-60908	Sequence	60908, A
40	52	63.4	217	4	US-10-424-599-271036	Sequence	271036,
41	52	63.4	306	4	US-10-425-114-51732	Sequence	51732, A
42	52	63.4	398	4	US-10-425-114-55344	Sequence	55344, A
43	52	63.4	410	4	US-10-424-599-271035	Sequence	•
44	52	63.4	416	4	US-10-437-963-188385	Sequence	•
45	52	63.4	417	4	US-10-424-599-271037	Sequence	•
46	52	63.4	420	4	US-10-424-599-257607	Sequence	•
47	52	63.4	420	4	US-10-424-599-257608	Sequence	•
48	52	63.4	420	4	US-10-437-963-128712	Sequence	•
49			420	4		•	•
	52	63.4		_	US-10-425-115-332061	Sequence	
50	52	63.4	424	4	US-10-425-114-46242	•	46242, A
51	52	63.4	433	4	US-10-425-114-63266	•	63266, A
52	52	63.4	435	4	US-10-425-114-59462	•	59462, A
53	52	63.4	435	4	US-10-425-114-65366	•	65366, A
54	51	62.2	338	6	US-11-096-568A-21865	•	21865, A
55	51	62.2	342	4	US-10-425-114-68558	•	68558, A
56	51	62.2	419	4	US-10-437-963-194308	Sequence	
57	51	62.2	419	4	US-10-767-701-47403	Sequence	47403, A
58	51	62.2	419	4	US-10-425-115-266771	Sequence	266771,
59	51	62.2	419	4	US-10-425-115-266773	Sequence	266773,
60	51	62.2	419	4	US-10-425-115-266781	Sequence	266781,
61	51	62.2	419	4	US-10-425-115-305086	Sequence	305086,
62	51	62.2	419	6	US-11-096-568A-21864	-	21864, A
						•	•

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-16.rapbn.

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Run on:

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

June 2, 2006, 19:30:30; Search time 3.57616 Seconds

(without alignments)

48.509 Million cell updates/sec

Title: US-10-001-938-16

Perfect score: 82

1 PGMVQQIQSVCMECQ 15 Sequence:

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

58871 seqs, 11565156 residues Searched:

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 1000 summaries

Published_Applications_AA_New:* Database :

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:* 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10 NEW PUB.pep:* 7: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11 NEW PUB.pep:* 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

No.	Score	Match	Length	DB	ID	Description
1	82	100.0	15	6	US-10-490-949-25	Sequence 25, Appl
2	71	86.6	397	7	US-11-293-697-3837	Sequence 3837, Ap
3	71	86.6	426	7	US-11-293-697-4751	Sequence 4751, Ap
4	55	67.1	257	6	US-10-953-349-1056	Sequence 1056, Ap
5	55	67.1	337	6	US-10-953-349-1055	Sequence 1055, Ap
6	55	67.1	419	6	US-10-953-349-1054	Sequence 1054, Ap
7	52	63.4	338	6	US-10-953-349-13711	Sequence 13711, A
8	52	63.4	382	6	US-10-953-349-13710	Sequence 13710, A
9	52	63.4	420	6	US-10-953-349-13709	Sequence 13709, A
10	50	61.0	256		US-10-953-349-16379	Sequence 16379, A
11	50	61.0	336		US-10-953-349-16378	Sequence 16378, A
12	50	61.0	417	6	US-10-953-349-16377	Sequence 16377, A
13	39	47.6	63	6	US-10-953-349-27957	Sequence 27957, A
14	38.5	47.0	1822	6	US-10-505-928-700	Sequence 700, App
15	38	46.3	708	6	US-10-505-928-416	Sequence 416, App
16	37	45.1	171	6	US-10-953-349-36964	Sequence 36964, A
17	37	45.1	183	6	US-10-953-349-36963	Sequence 36963, A
18	37 27	45.1	206	6	US-10-953-349-35898	Sequence 35898, A
19 20	37 37	45.1 45.1	234 246	6 6	US-10-505-928-152 US-10-953-349-35897	Sequence 152, App Sequence 35897, A
21	37	45.1	300		US-10-953-349-35896	Sequence 35896, A
22	36	43.1	112		US-11-293-697-3203	Sequence 3203, Ap
23	36	43.9	117	7	US-11-219-121-11	Sequence 11, Appl
24	36	43.9	146		US-11-219-121-13	Sequence 13, Appl
25	36	43.9	341	6	US-10-953-349-17124	Sequence 17124, A
26	36	43.9	352		US-10-953-349-17123	Sequence 17123, A
27	36	43.9	437	6	US-10-953-349-17122	Sequence 17122, A
28	36	43.9	790	-	US-10-511-937-2937	Sequence 2937, Ap
29	35	42.7	141	7	US-11-293-697-2640	Sequence 2640, Ap
30	35	42.7	420	7	US-11-232-370-7	Sequence 7, Appli
31	35	42.7	524	7	US-11-232-370-12	Sequence 12, Appl
32	35	42.7	525	7	US-11-232-370-13	Sequence 13, Appl
33	35	42.7	525	7	US-11-232-370-14	Sequence 14, Appl
34	35	42.7	543	7	US-11-232-370-6	Sequence 6, Appli
35	35	42.7	544	7	US-11-232-370-9	Sequence 9, Appli
36	35	42.7	544	7	US-11-232-370-11	Sequence 11, Appl
37	35	42.7	545	7	US-11-232-370-8	Sequence 8, Appli
38	35	42.7	559	7	US-11-232-370-10	Sequence 10, Appl
39	35	42.7	660		US-10-953-349-10967	Sequence 10967, A
40	34	41.5	25	7	US-11-219-563-115	Sequence 115, App
41	34	41.5	82		US-11-219-563-119	Sequence 119, App
42	34	41.5	91	6	US-10-514-263-7	Sequence 7, Appli
43	34	41.5	108	7	US-11-328-747-6	Sequence 6, Appli
44	34	41.5	109		US-10-953-349-7536	Sequence 7536, Ap
45	34	41.5 41.5			US-10-953-349-7535 US-10-506-063A-14	Sequence 7535, Ap Sequence 14, Appl
46 47	34 34	41.5	119		US-10-953-349-39848	Sequence 39848, A
48	34	41.5	119		US-10-953-349-39911	Sequence 39911, A
49	34	41.5	121		US-11-219-563-84	Sequence 84, Appl
50	34	41.5	121		US-11-219-563-89	Sequence 89, Appl
51	34	41.5	121		US-11-219-563-90	Sequence 90, Appl
52	34	41.5	125		US-10-953-349-29673	Sequence 29673, A
53	34	41.5			US-10-953-349-39847	Sequence 39847, A
54	34	41.5	145		US-10-953-349-39909	Sequence 39909, A
55	34	41.5	153		US-10-953-349-29671	Sequence 29671, A
56	34	41.5	164		US-10-953-349-12472	Sequence 12472, A
57	34	41.5	196		US-10-953-349-12471	Sequence 12471, A
58	34	41.5	202	6	US-10-953-349-16651	Sequence 16651, A
59	34	41.5	230	6	US-10-953-349-32248	Sequence 32248, A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-17.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 17.rai.

<u>start</u>

Go Back to previc

GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

June 2, 2006, 19:08:52; Search time 11.4238 Seconds Run on:

(without alignments)

114.932 Million cell updates/sec

Title: US-10-001-938-17

Perfect score: 76

Sequence: 1 GRRITTRRIMENGQE 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

650591 seqs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:* 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:* 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:* 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:* /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length DB ID			Description
1 2		100.0	277 277		US-08-868-288A-7 US-09-235-373-7	Sequence 7, Appli Sequence 7, Appli

2	76	100.0	277	2	110 00-200-002-7	Comionao	7 Appli
3	76			_	US-09-388-993-7 US-09-501-714-7	Sequence	
4	76	100.0	277	2		Sequence	
5	76 76	100.0	327	2	US-09-949-016-11262	Sequence	•
6	76	100.0	351	1	US-08-868-288A-6	Sequence	
7	76	100.0	351	2	US-09-235-373-6	Sequence	
8	76	100.0	351	2	US-09-388-993-6	Sequence	
9	76	100.0	351	2	US-09-501-714-6	Sequence	
10	66	86.8	330	1	US-08-868-288A-3	Sequence	
11	66	86.8	330	2	US-09-235-373-3	Sequence	
12	66	86.8	330	2	US-09-388-993-3	Sequence	
13	66	86.8	330	2	US-09-501-714-3	Sequence	3, Appli
14	45	59.2	379	2	US-09-967-552A-2	Sequence	2, Appli
15	45	59.2	379	2	US-09-967-552A-26	Sequence	26, Appl
16	45	59.2	379	2	US-09-967-552A-30	Sequence	30, Appl
17	45	59.2	391	2	US-09-967-552A-18	Sequence	18, Appl
18	41	53.9	405	2	US-09-134-000C-4680	Sequence	4680, Ap
19	41	53.9	867	2	US-09-668-673B-2	Sequence	2, Appli
20	41	53.9	867	2	US-10-389-532-2	Sequence	- -
21	41	53.9	1558	2	US-09-949-016-6803	Sequence	
22	41	53.9	1606	2	US-09-949-016-7371	Sequence	
23	40	52.6	207	2	US-09-248-796A-15834	Sequence	•
24	40	52.6	268	2	US-09-270-767-44519	Sequence	
		51.3	178	2	US-09-107-532A-3960	•	•
25	39			_		Sequence	_
26	39	51.3	184	2	US-09-198-452A-1138	Sequence	•
27	39	51.3	315	2	US-09-438-185A-26	Sequence	• •
28	38	50.0	130	2	US-09-489-039A-11337	Sequence	ľ
29	38	50.0	165	2	US-09-902-540-15997	Sequence	7
30	38	50.0	414	2	US-09-252-991A-27975	Sequence	•
31	38	50.0	455	2	US-09-902-540-11484	Sequence	•
32	38	50.0	473	2	US-09-489-039A-9737	Sequence	9737, Ap
33	38	50.0	764	2	US-09-585-858-15	Sequence	15, Appl
34	38	50.0	764	2	US-10-270-878-15	Sequence	15, Appl
35	38	50.0	837	1	US-08-680-326-117	Sequence	117, App
36	38	50.0	1008	1	US-08-680-326-30	Sequence	30, Appl
37	38	50.0	1009	1	US-08-680-326-31	Sequence	31, Appl
38	38	50.0	1037	2	US-09-902-540-9845	Sequence	9845, Ap
39	38	50.0	1341	2	US-09-252-991A-26785	Sequence	26785, A
40	37	48.7	375	2	US-09-303-518D-632	Sequence	
41	37	48.7	375	2	US-09-303-518D-634	Sequence	• •
42	37	48.7	544	2	US-09-252-991A-28995	Sequence	
43	36	47.4	92	2	US-09-902-540-13452	Sequence	
44	36	47.4	165	2	US-09-252-991A-31768	Sequence	· ·
45	36	47.4	233	2	US-09-489-039A-9119	Sequence	·
46	36	47.4	301	2	US-09-252-991A-22565	Sequence	•
47	36	47.4	314	2	US-09-252-991A-26728	Sequence	
		47.4	355	2	US-09-328-352-6270	•	6270, Ap
48	36					-	114, App
49	36	47.4	498	2	US-09-477-962-114	-	
50	36	47.4	610	2	US-09-248-796A-17030	Sequence	·
51	36	47.4	636	2	US-09-489-039A-13947	Sequence	
52	36	47.4	651	2	US-09-371-338-15	•	15, Appl
53	36	47.4	703	2	US-10-116-326-6	Sequence	
54	36	47.4	703	2	US-10-803-277-6	•	6, Appli
55	36	47.4	762	2	US-10-116-326-4	Sequence	
56	36	47.4	762	2	US-10-803-277-4	-	4, Appli
57	36	47.4	778	2	US-10-116-326-2	Sequence	
58	36	47.4	778	2	US-10-003-690-2	Sequence	
59	36	47.4	778	2	US-10-803-277-2	Sequence	2, Appli
60	36	47.4	898	1	US-08-465-995A-4	Sequence	4, Appli
61	36	47.4	898	1	US-08-465-994C-4	Sequence	4, Appli
62	36	47.4	898	1	US-08-966-145-4	Sequence	4, Appli
63	36	47.4	920	1	US-08-101-593-4	Sequence	4, Appli
-	-					•	

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-17.rapbm.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 17.rapbm.

<u>start</u>

Go Back to prev

GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2006, 19:29:53; Search time 75.9934 Seconds

(without alignments)

91.432 Million cell updates/sec

Title: US-10-001-938-17

Perfect score: 76

1 GRRITTRRIMENGQE 15 Sequence:

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

2097797 seqs, 463214858 residues Searched:

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 1000 summaries

Published Applications AA Main:* Database :

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

કુ Result Query No. Score Match Length DB ID Description 76 100.0 15 4 US-10-001-938-17 Sequence 17, Appl

2	66	86.8	242	4	US-10-264-049-2674	_	2674, Ap
3	63	82.9	164	4	US-10-363-829-341	-	341, App
4	63	82.9	227	4	US-10-220-120-322	Sequence	
5	60	78.9	232	5	US-10-480-988-22	Sequence	22, Appl
6	60	78.9	267	3	US-09-764-868-1164	Sequence	1164, Ap
7	60	78.9	267	3	US-09-764-891-4089	Sequence	4089, Ap
8	45	59.2	338	6	US-11-188-298-15117	Sequence	15117, A
9	45	59.2	379	3	US-09-967-552A-2	Sequence	2, Appli
10	45	59.2	379	3	US-09-967-552A-26	Sequence	26, Appl
11	45	59.2	379	3	US-09-967-552A-30	Sequence	• • •
12	45	59.2	379	5	US-10-965-357-2	-	2, Appli
13	45	59.2	379	5	US-10-965-357-26	Sequence	
14	45	59.2	379	5	US-10-965-357-30	-	30, Appl
15	45	59.2	379	5	US-10-967-851-2	-	2, Appli
16	45	59.2	379	5	US-10-967-851-26	-	26, Appl
17	45	59.2	379	5	US-10-967-851-20	-	30, Appl
				_		-	
18	45	59.2	379	6	US-11-188-298-9209	-	9209, Ap
19	45	59.2	379	6	US-11-188-298-12077	•	12077, A
20	45	59.2	379	6	US-11-188-298-13625	•	13625, A
21	45	59.2	379	6	US-11-188-298-17015	•	17015, A
22	45	59.2	380	3	US-09-906-549-2	•	2, Appli
23	45	59.2	380	6	US-11-188-298-2231	Sequence	2231, Ap
24	45	59.2	380	6	US-11-188-298-15608	Sequence	15608, A
25	45	59.2	388	4	US-10-425-115-347505	Sequence	347505,
26	45	59.2	391	3	US-09-967-552A-18	Sequence	18, Appl
27	45	59.2	391	5	US-10-965-357-18	Sequence	18, Appl
28	45	59.2	391	5	US-10-967-851-18	Sequence	18, Appl
29	45	59.2	443	5	US-10-739-930-8161	Sequence	8161, Ap
30	45	59.2	453	4	US-10-425-114-65489	Sequence	65489, A
31	44	57.9	379	4	US-10-767-701-44558	Sequence	44558, A
32	43	56.6	137	4	US-10-437-963-156565	Sequence	
33	43	56.6	143	4	US-10-425-115-337503	Sequence	
34	43	56.6	375	4	US-10-424-599-271970	Sequence	
35	42	55.3	78	4	US-10-425-115-290387	Sequence	
36	42	55.3	202	4	US-10-425-114-47897	_	47897, A
37	42	55.3	427	4	US-10-425-114-45447	•	45447, A
38	42	55.3	563	4	US-10-425-115-286927	Sequence	-
39	42	55.3	568	4	US-10-425-115-263963	Sequence	-
40	42	55.3	591	4	US-10-425-114-61059	-	61059, A
41	42	55.3	699	4	US-10-437-963-192225	Sequence	•
42	42	55.3	2391	4	US-10-425-115-245853	Sequence	_
		53.9	2331 77	3	US-09-989-890-171	-	171, App
43	41			3 4		Sequence	
44	41	53.9	98 967	_	US-10-437-963-202081	-	
45	41 41	53.9	867	4	US-10-389-532-2	-	2, Appli
46	• •	53.9	1845	4	US-10-408-765A-1351		1351, Ap
47	40	52.6	264	6	US-11-097-143-42933	-	42933, A
48	40	52.6	404	4	US-10-437-963-117500	Sequence	
49	40	52.6	416	4	US-10-425-114-65332	_	65332, A
50	40	52.6	625	5	US-10-739-930-5867	•	5867, Ap
51	40	52.6	1061	4	US-10-369-493-12847	•	12847, A
52	40	52.6	8805	6	US-11-097-143-28128	•	28128, A
53	39	51.3	38	4	US-10-425-115-242521	Sequence	
54	39	51.3	92	4	US-10-437-963-113613	Sequence	•
55	39	51.3	108	4	US-10-767-701-34584	•	34584, A
56	39	51.3	184	4	US-10-289-762-1138	•	1138, Ap
57	39	51.3	191	3	US-09-733-507-2	•	2, Appli
58	39	51.3	210	4	US-10-424-599-203088	Sequence	203088,
59	39	51.3	456	4	US-10-425-114-51670	Sequence	51670, A
60	39	51.3	671	4	US-10-282-122A-76971	Sequence	76971, A
61	39	51.3	773	4	US-10-437-963-121782	Sequence	121782,
62	39	51.3	1450	4	US-10-437-963-110511	Sequence	110511,

SCORE Search Results Details for Application 10 and Search Result us-10-001-938-17.rapb

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 start

Go Bac

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OM protein - protein search, using sw model

June 2, 2006, 19:30:30; Search time 3.57616 Seconds Run on:

(without alignments)

48.509 Million cell updates/sec

Title: US-10-001-938-17

Perfect score: 76

1 GRRITTRRIMENGQE 15 Sequence:

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

58871 seqs, 11565156 residues Searched:

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Published Applications_AA_New: * Database :

/EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:* 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 NEW_PUB.pep:* 5: /EMC Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:* 7: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description		
1	76	100.0		_	US-10-490-949-26	Sequence 26, Appl		
2	41	53.9	867	7	US-11-316-132-3	Sequence 3, Appli		

3	36	47.4	18	7	US-11-251-734-28	_	28, Appl
4	36	47.4	174	6	US-10-953-349-28370	Sequence	28370, A
5	35	46.1	166	6	US-10-953-349-30966	Sequence	30966, A
6	35	46.1	212	6	US-10-953-349-30965	Sequence	30965, A
7	35	46.1	289	7	US-11-293-697-4302	Sequence	4302, Ap
8	35	46.1	293	6	US-10-953-349-30964	Sequence	30964, A
9	35	46.1	870	7	US-11-316-132-4	Sequence	4, Appli
10	34	44.7	207	6	US-10-953-349-28505	Sequence	28505, A
11	34	44.7	233	6	US-10-953-349-28504	Sequence	28504, A
12	34	44.7	336	6	US-10-953-349-28503	Sequence	28503, A
13	34	44.7	355	6	US-10-953-349-19922	Sequence	19922, A
14	34	44.7	362	6	US-10-511-937-2509	Sequence	2509, Ap
15	34	44.7	363	6	US-10-953-349-19921	Sequence	19921, A
16	34	44.7	365	6	US-10-511-937-2530	Sequence	2530, Ap
17	34	44.7	372	7	US-11-319-606-3	•	3, Appli
18	34	44.7	381	6	US-10-953-349-19920	•	19920, A
19	33	43.4	154	6	US-10-953-349-33149	•	33149, A
20	33	43.4	362	6	US-10-953-349-26895	_	26895, A
21	33	43.4	375	6	US-10-953-349-26894	_	26894, A
22	33	43.4	619	7	US-11-312-958-46	•	46, Appl
23	33	43.4	730	6	US-10-505-928-841	•	841, App
24	33	43.4	870	7	US-11-316-132-2	-	2, Appli
25	33	43.4	871	7	US-11-316-132-1	•	1, Appli
26	32.5	42.8	985	7	US-11-342-171-6	-	6, Appli
27	32.5	42.8	985	7	US-11-342-171-66		66, Appl
28	32.3	42.1	212	6	US-10-953-349-5598	-	5598, Ap
29	32	42.1	221	6	US-10-953-349-5597	-	5597, Ap
30	32	42.1	221	6	US-10-953-349-4194	-	4194, Ap
				6	US-10-953-349-4194 US-10-953-349-5596	-	•
31	32	42.1	240	•		•	5596, Ap
32	32	42.1	328	6	US-10-953-349-24057	•	24057, A
33	32	42.1	358	6	US-10-953-349-17279	•	17279, A
34	32	42.1	363	6	US-10-953-349-31909		31909, A
35	32	42.1	366	6	US-10-953-349-17278	•	17278, A
36	32	42.1	366	6	US-10-953-349-31908	_	31908, A
37	32	42.1	368	6	US-10-953-349-31907	_	31907, A
38	32	42.1	375	6	US-10-953-349-24056	•	24056, A
39	32	42.1	377	6	US-10-953-349-17277	•	17277, A
40	32	42.1	429	6	US-10-953-349-24055	•	24055, A
41	32	42.1	563	7	US-11-238-282-33	-	33, Appl
42	32	42.1	682	6	US-10-953-349-11676	•	11676, A
43	32	42.1	1018	7	US-11-293-697-2998	-	2998, Ap
44	31.5	41.4	604	6	US-10-953-349-7849	-	7849, Ap
45	31.5	41.4	623	6	US-10-953-349-7848	•	7848, Ap
46	31.5	41.4	675	6	US-10-953-349-7847	-	7847, Ap
47	31	40.8	150	6	US-10-953-349-27238		27238, A
48	31	40.8	209	6	US-10-953-349-11931	-	11931, A
49	31	40.8	210	6	US-10-953-349-11930	-	11930, A
50	31	40.8	246	6	US-10-953-349-17768	_	17768, A
51	31	40.8	247	6	US-10-953-349-17767	•	17767, A
52	31	40.8	255	7	US-11-293-697-4175	Sequence	4175, Ap
53	31	40.8	302	6	US-10-953-349-7938	Sequence	7938, Ap
54	31	40.8	311	6	US-10-953-349-7937	Sequence	7937, Ap
55	31	40.8	326	6	US-10-953-349-7936	Sequence	7936, Ap
56	31	40.8	340	7	US-11-271-287-34	Sequence	34, Appl
57	31	40.8	362	6	US-10-511-937-2608	Sequence	2608, Ap
58	31	40.8	371	6	US-10-953-349-5963	Sequence	5963, Ap
59	31	40.8	372	6	US-10-953-349-5962	Sequence	5962, Ap
60	31	40.8	374	6	US-10-953-349-5961	Sequence	5961, Ap
61	31	40.8	441	6	US-10-953-349-31759	Sequence	31759, A
62	31	40.8	452	6	US-10-953-349-34342	Sequence	34342, A
63	31	40.8	504	6	US-10-953-349-3846	-	3846, Ap
						-	•

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-18.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 18.rai.

start

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

June 2, 2006, 19:08:52; Search time 12.1854 Seconds Run on:

(without alignments)

114.932 Million cell updates/sec

US-10-001-938-18 Title:

Perfect score: 80

Sequence: 1 QAYEVLSDAKKRELYD 16

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

650591 seqs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

1: /EMC Celerra SIDS3/ptodata/2/iaa/5_COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/iaa/7_COMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:* 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

/EMC Celerra SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1 2		100.0	102 127		US-09-513-999C-5137 US-09-370-838-199	Sequence 5137, Ap Sequence 199, App

3	80	100.0	127	2	US-09-854-133-199	Sequence	199, App
4	80	100.0	397	1	US-08-868-288A-5	Sequence	5, Appli
5	80	100.0	397	2	US-09-235-373-5	Sequence	5, Appli
6	80	100.0	397	2	US-09-388-993-5	Sequence	5, Appli
7	80	100.0	397	2	US-09-919-039-178	Sequence	
8	80	100.0	397	2	US-09-538-092-1052	•	• •
				_		Sequence	· -
9	80	100.0	397	2	US-09-501-714-5	Sequence	• • •
10	72	90.0	330	1	US-08-868-288A-3	Sequence	3, Appli
11	72	90.0	330	2	US-09-235-373-3	Sequence	3, Appli
12	72	90.0	330	2	US-09-388-993-3	Sequence	3, Appli
13	72	90.0	330	2	US-09-501-714-3	Sequence	3, Appli
14	70	87.5	334	3	US-10-429-223-3	Sequence	• •
15	70	87.5	337	2	US-09-665-479A-8	Sequence	• •
				3	US-10-429-223-2		
16	70	87.5	397	-		Sequence	
17	70	87.5	397	3	US-10-429-223-4	Sequence	
18	69	86.2	419	1	US-08-686-417-3	Sequence	3, Appli
19	64	80.0	152	2	US-09-270-767-46278	Sequence	46278, A
20	64	80.0	277	1	US-08-868-288A-7	Sequence	7, Appli
21	64	80.0	277	2	US-09-235-373-7	Sequence	7, Appli
22	64	80.0	277	2	US-09-388-993-7	Sequence	
23	64	80.0	277	2	US-09-501-714-7	Sequence	
				_		-	
24	64	80.0	327	2	US-09-949-016-11262	Sequence	•
25	64	80.0	351	1	US-08-868-288A-6	Sequence	6, Appli
26	64	80.0	351	2	US-09-235-373-6	Sequence	6, Appli
27	64	80.0	351	2	US-09-388-993-6	Sequence	6, Appli
28	64	80.0	351	2	US-09-501-714-6	Sequence	6, Appli
29	62	77.5	348	1	US-08-974-546-1	Sequence	
30	62	77.5	375	2	US-09-328-352-4984	Sequence	
		77.5	397	2	US-09-248-796A-17628	Sequence	-
31	62					-	
32	61	76.2	75	2	US-09-513-999C-6016	Sequence	•
33	61	76.2	381	2	US-09-252-991A-27174	Sequence	-
. 34	60	75.0	51	1	US-08-346-849-12	Sequence	12, Appl
35	60	75.0	51	1	US-08-293-284A-12	Sequence	12, Appl
36	60	75.0	51	2	US-08-898-300-12	Sequence	12, Appl
37	60	75.0	51	2	US-08-824-513-12	Sequence	
38	60	75.0	340	1	US-08-974-546-5	Sequence	
39	60	75.0	340	2	US-09-949-016-6691	Sequence	
				_		-	•
40	60	75.0	363	2	US-09-949-016-8899	Sequence	•
41	60	75.0	391	2	US-09-902-540-11110	Sequence	•
42	59	73.8	392	2	US-09-198-452A-48	Sequence	48, Appl
43	59	73.8	406	2	US-09-438-185A-34	Sequence	34, Appl
44	58	72.5	49	1	US-08-346-849-11	Sequence	11, Appl
45	58	72.5	49	1	US-08-293-284A-11	Sequence	11, Appl
46	58	72.5	49	2	US-08-898-300-11	Sequence	
47	58	72.5	49	2	US-08-824-513-11	Sequence	
48	58	72.5	286	2	US-09-248-796A-16992	Sequence	· • •
						-	
49	58	72.5	358	1	US-08-868-288A-1	Sequence	- -
50	58	72.5	358	2	US-09-235-373-1	Sequence	
51	58	72.5	358	2	US-09-388-993-1	Sequence	1, Appli
52	58	72.5	358	2	US-09-991-181-148	Sequence	148, App
53	58	72.5	358	2	US-09-501-714-1	Sequence	1, Appli
54	58	72.5	358	2	US-09-990-444-148	Sequence	148, App
55	58	72.5	358	2	US-09-997-333-148	Sequence	
56	58	72.5	358	2	US-09-992-598-148	Sequence	
57		72.5	358	2	US-09-989-735-148	Sequence	
	58					_	
58	58	72.5	358	3	US-09-989-726-148	Sequence	
59	58	72.5	358	3	US-09-997-514-148	Sequence	
60	58	72.5	358	3	US-09-989-728-148	Sequence	
61	58	72.5	358	3	US-09-997-349-148	Sequence	148, App
62	58	72.5	358	3	US-09-997-653-148	Sequence	148, App
63	58	72.5	358	3	US-09-989-293A-148	Sequence	
	-					•	- •

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938 18.rapbm.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

June 2, 2006, 19:29:53; Search time 81.0596 Seconds Run on:

(without alignments)

91.432 Million cell updates/sec

US-10-001-938-18 Title:

Perfect score: 80

1 QAYEVLSDAKKRELYD 16 Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

2097797 seqs, 463214858 residues Searched:

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 1000 summaries

Published Applications AA Main: * Database :

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 PUBCOMB.pep:* 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query No. Score Match Length DB ID Description 80 100.0 16 4 US-10-001-938-18 Sequence 18, Appl 1

_				_			
2	80	100.0	127	3	US-09-738-973-199	Sequence	199, App
3	80	100.0	127	3	US-09-854-133-199	Sequence	199, App
4	80	100.0	127	4	US-10-144-649A-199	Sequence	199, App
5	80	100.0	252	4	US-10-264-049-4191	Sequence	4191, Ap
6	80	100.0	397	3	US-09-919-039-178	Sequence	178, App
7	80	100.0	397	5	US-10-473-127-1138	•	1138, Ap
8	80	100.0	397	5	US-10-473-127-1139	-	1139, Ap
9	80	100.0	397	5	US-10-473-127-1140	-	1140, Ap
10	80	100.0	397	5	US-10-473-127-1143	-	- · · · · · · · · · · · · · · · · · · ·
				-		-	1143, Ap
11	80	100.0	397	5	US-10-473-127-1144	•	1144, Ap
12	80	100.0	397	5	US-10-473-127-1145	-	1145, Ap
13	80	100.0	397	5	US-10-756-149-4727	Sequence	4727, Ap
14	80	100.0	397	5	US-10-631-467-559	Sequence	559, App
15	80	100.0	397	5	US-10-878-556A-155	Sequence	155, App
16	80	100.0	408	5	US-10-450-763-40099	Sequence	40099, A
17	74	92.5	397	5	US-10-631-467-1386	Sequence	1386, Ap
18	73	91.2	105	4	US-10-425-115-295507	Sequence	•
19	72	90.0	242	4	US-10-264-049-2674	-	2674, Ap
20	70	87.5	334	4	US-10-429-223-3	-	3, Appli
				_		_	
21	70	87.5	337	4	US-10-788-792-162	-	162, App
22	70	87.5	397	4	US-10-429-223-2		2, Appli
23	70	87.5	397	4	US-10-429-223-4		4, Appli
24	69	86.2	59	4	US-10-425-115-337846	Sequence	337846,
25	69	86.2	103	4	US-10-425-115-205457	Sequence	205457,
26	69	86.2	153	4	US-10-425-115-295502	Sequence	295502,
27	69	86.2	167	4	US-10-767-701-39847	Sequence	39847, A
28	69	86.2	183	4	US-10-425-115-295514	Sequence	· ·
29	69	86.2	192	4	US-10-425-115-295500	Sequence	·
30	69	86.2	194	4	US-10-425-115-295516	Sequence	•
31	69	86.2	211	4		•	•
				_	US-10-767-701-47401	•	47401, A
32	69	86.2	212	4	US-10-425-115-309309	Sequence	•
33	69	86.2	217	4	US-10-424-599-271036	Sequence	•
34	69	86.2	232	5	US-10-480-988-22	Sequence	22, Appl
35	69	86.2	267	3	US-09-764-868-1164	Sequence	1164, Ap
36	69	86.2	267	3	US-09-764-891-4089	Sequence	4089, Ap
37	69	86.2	363	4	US-10-425-115-304214	Sequence	304214,
38	69	86.2	397	4	US-10-108-260A-3837	Sequence	3837, Ap
39	69	86.2	410	4	US-10-424-599-271035	Sequence	•
40	69	86.2	417	4	US-10-424-599-186616	Sequence	•
41	69	86.2	417	4	US-10-424-599-271037	Sequence	•
42	69	86.2	417	4	US-10-437-963-194306	Sequence	-
43		86.2		4		_	•
	69		417	_	US-10-425-115-307680	Sequence	•
44	69	86.2	418	4	US-10-425-115-307678	Sequence	•
45	69	86.2	418	4	US-10-425-115-307679	Sequence	
46	69	86.2	419	4	US-10-437-963-194308	Sequence	194308,
47	69	86.2	419	4	US-10-767-701-47403	Sequence	47403, A
48	69	86.2	419	4	US-10-425-115-266771	Sequence	266771,
49	69	86.2	419	4	US-10-425-115-266773	Sequence	266773,
50	69	86.2	419	4	US-10-425-115-266781	Sequence	266781,
51	69	86.2	419	4	US-10-425-115-305086	Sequence	•
52	69	86.2	419	6	US-11-096-568A-21864	_	21864, A
53	69	86.2	420	4	US-10-425-115-266776	Sequence	•
54	69	86.2	421	4	US-10-425-113-286776 US-10-425-114-63525	•	•
						•	63525, A
55 56	69	86.2	426	4	US-10-108-260A-4751	•	4751, Ap
56 57	69	86.2	433	4	US-10-425-114-60908	•	60908, A
57	69	86.2	449	4	US-10-425-114-62758	•	62758, A
58	69	86.2	449	4	US-10-425-114-63503	•	63503, A
59	69	86.2	449	4	US-10-425-114-65975	Sequence	65975, A
60	69	86.2	449	4	US-10-425-114-73027	Sequence	73027, A
61	69	86.2	450	4	US-10-425-114-46482	Sequence	46482, A
62	69	86.2	450	4	US-10-425-114-51073	_	51073, A
						•	•

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-18.rapbn.

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OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:30:30; Search time 3.81457 Seconds

(without alignments)

48.509 Million cell updates/sec

Title:

US-10-001-938-18

Perfect score: 80

Sequence:

1 QAYEVLSDAKKRELYD 16

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched:

58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seg length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New:*

/EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10 NEW PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /EMC Celerra SIDS3/ptodata/2/pubpaa/US60 NEW PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

ક્ર

No.	Score	Match	Length	DB	ID	Description
1	80	100.0	16	6	US-10-490-949-27	Sequence 27, Appl
2	69	86.2	397	7	US-11-293-697-3837	Sequence 3837, Ap
3	69	86.2	417	6	US-10-953-349-16377	Sequence 16377, A
4	69	86.2	419	6	US-10-953-349-1054	Sequence 1054, Ap
5	69	86.2	426	7	US-11-293-697-4751	Sequence 4751, Ap
6	66	82.5	156	6	US-10-953-349-28215	Sequence 28215, A
7	66	82.5	190	6	US-10-953-349-28214	Sequence 28214, A
8	66	82.5	191	6	US-10-953-349-28213	Sequence 28213, A
9	65	81.2	382	6	US-10-953-349-13710	Sequence 13710, A
10	65	81.2	420	6	US-10-953-349-13709	Sequence 13709, A
11	64	80.0	16	6	US-10-490-949-28	Sequence 28, Appl
12	62	77.5	308	6	US-10-953-349-33811	Sequence 33811, A
13	62	77.5	336	6	US-10-953-349-33810	Sequence 33810, A
14	62	77.5	430	6	US-10-953-349-33809	Sequence 33809, A
15	59	73.8	332	6	US-10-953-349-1407	Sequence 1407, Ap
16	59	73.8	367	6	US-10-953-349-1406	Sequence 1406, Ap
17	59	73.8	456	6	US-10-953-349-1405	Sequence 1405, Ap
18	57 - -	71.2	321	6	US-10-953-349-950	Sequence 950, App
19	57 - -	71.2	323	6	US-10-953-349-949	Sequence 949, App
20	57	71.2	349	6	US-10-953-349-948	Sequence 948, App
21	57	71.2	380	6	US-10-953-349-7175	Sequence 7175, Ap
22	57	71.2	391	6	US-10-953-349-7174	Sequence 7174, Ap
23	57	71.2	442	6	US-10-953-349-7173	Sequence 7173, Ap
24	54	67.5	189	7	US-11-293-697-4556	Sequence 4556, Ap
25	54	67.5	389	7	US-11-122-986-185	Sequence 185, App
26	54	67.5	389	7	US-11-122-986-187	Sequence 187, App
27	54	67.5	583	6	US-10-953-349-35418	Sequence 35418, A
28	54	67.5	630	6	US-10-953-349-35417	Sequence 35417, A
29	53	66.2	307	6	US-10-953-349-2183	Sequence 2183, Ap
30	53	66.2	335	6	US-10-953-349-2182	Sequence 2182, Ap
31	53	66.2	343	6	US-10-953-349-2181	Sequence 2181, Ap
32	52	65.0	60	6	US-10-953-349-31081	Sequence 31081, A
33 34	52 52	65.0	95	6	US-10-953-349-31080	Sequence 31080, A
35	52 52	65.0 65.0	119 119	6 6	US-10-953-349-5019	Sequence 5019, Ap
36	52 52	65.0	147	6	US-10-953-349-28161 US-10-953-349-28160	Sequence 28161, A
37	52 52	65.0	155	6	US-10-953-349-28159	Sequence 28160, A Sequence 28159, A
38	52	65.0	156	6	US-10-953-349-20139	Sequence 5018, Ap
39	52	65.0	530	6	US-10-953-349-20585	Sequence 20585, A
40	51	63.7	339	6	US-10-953-349-12422	Sequence 12422, A
41	51	63.7	379	6	US-10-953-349-11645	Sequence 11645, A
42	51	63.7	468	6	US-10-953-349-32244	Sequence 32244, A
43	51	63.7	486	6	US-10-953-349-32243	Sequence 32243, A
44	50	62.5	391	6	US-10-953-349-7627	Sequence 7627, Ap
45	49	61.3	340	6	US-10-953-349-24393	Sequence 24393, A
46	49	61.3	427	6	US-10-953-349-24392	Sequence 24392, A
47	49	61.3	445	6	US-10-953-349-24391	Sequence 24391, A
48	47	58.8	305	6	US-10-953-349-23847	Sequence 23847, A
49	45	56.2	260	7	US-11-293-697-2489	Sequence 2489, Ap
50	44	55.0	160	6	US-10-953-349-6860	Sequence 6860, Ap
51	44	55.0	199	6	US-10-953-349-9116	Sequence 9116, Ap
52	44	55.0	248	6	US-10-953-349-9115	Sequence 9115, Ap
53	43	53.8	161	6	US-10-953-349-37092	Sequence 37092, A
54	43	53.8	190	6	US-10-953-349-37091	Sequence 37091, A
55	42	52.5	138	6	US-10-953-349-20728	Sequence 20728, A
56	42	52.5	158	6	US-10-953-349-20727	Sequence 20727, A
57	42	52.5	159	6	US-10-953-349-20726	Sequence 20726, A
58	42	52.5	169	6	US-10-953-349-27713	Sequence 27713, A
59	42	52.5	465	6	US-10-953-349-8070	Sequence 8070, Ap

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-2.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 2.rai.

start

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

June 2, 2006, 19:08:52; Search time 11.4238 Seconds Run on:

(without alignments)

114.932 Million cell updates/sec

Title: US-10-001-938-2

Perfect score: 82

Sequence: 1 RKAYKRLAMKYHPDR 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

650591 seqs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

> 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:* 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:* 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:* 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:* 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:* 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:* /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
1	82	100.0	52	1	US-08-346-849-8	Sequence 8, Appli
2	82	100.0	52	1	US-08-293-284A-8	Sequence 8, Appli

•	0.0	100 0	5.0	_			
3	82	100.0	52	2	US-08-898-300-8	Sequence 8, Appl	
4	82	100.0	52	2	US-08-824-513-8	Sequence 8, Appl	i
5	82	100.0	131	2	US-09-553-498-4	Sequence 4, Appl	i
6	82	100.0	131	2	US-09-618-869-4	Sequence 4, Appl	i
7	82	100.0	399	2	US-09-553-498-2	Sequence 2, Appl	i
8	82	100.0	399	2	US-09-618-869-2	Sequence 2, Appl	
9	79	96.3	380	2	US-09-489-039A-9011	Sequence 9011, A	
10	76	92.7	380	2	US-09-543-681A-5912	Sequence 5912, A	_
11	76	92.7	381	2	US-09-252-991A-27174	Sequence 27174,	_
12	73	89.0	375	2	US-09-328-352-4984	_	
				_		Sequence 4984, A	-
13	68	82.9	376	3	US-10-375-010-22	Sequence 22, App	
14	67	81.7	87	2	US-09-882-835-4	Sequence 4, Appl	
15	67	81.7	102	2	US-09-513-999C-5137	Sequence 5137, A	_
16	67	81.7	127	2	US-09-370-838-199	Sequence 199, Ap	p
17	67	81.7	127	2	US-09-854-133-199	Sequence 199, Ap	p
18	67	81.7	397	1	US-08-868-288A-5	Sequence 5, Appl	i
19	67	81.7	397	2	US-09-235-373-5	Sequence 5, Appl	i
20	67	81.7	397	2	US-09-388-993-5	Sequence 5, Appl	
21	67	81.7	397	2	US-09-919-039-178	Sequence 178, Ap	
22	67	81.7	397	2	US-09-538-092-1052	Sequence 1052, A	_
23	67	81.7	397	2	US-09-501-714-5	Sequence 5, Appl	_
24	67	81.7	397	3	US-10-429-223-2		
				_		Sequence 2, Appl	
25	67	81.7	397	3	US-10-429-223-4	Sequence 4, Appl	
26	67	81.7	407	2	US-09-540-236-2899	Sequence 2899, A	-
27	66	80.5	392	2	US-09-198-452A-48	Sequence 48, App	
28	66	80.5	406	2	US-09-438-185A-34	Sequence 34, App	1
29	65	79.3	348	1	US-08-974-546-1	Sequence 1, Appl	i
30	63	76.8	52	1	US-08-346-849-10	Sequence 10, App	1
31	63	76.8	52	1	US-08-293-284A-10	Sequence 10, App	1
32	63	76.8	52	2	US-08-898-300-10	Sequence 10, App	1
33	63	76.8	52	2	US-08-824-513-10	Sequence 10, App	
34	63	76.8	96	2	US-09-621-976-4045	Sequence 4045, A	
35	63	76.8	147	2	US-09-270-767-33311	Sequence 33311,	-
36	63	76.8	147	2	US-09-270-767-48528	Sequence 48528,	
37	63	76.8	147	2	US-09-513-999C-6925	Sequence 6925, A	
38	63	76.8	223	2	US-09-658-644-4		-
						Sequence 4, Appl	
39	63	76.8	223	2	US-09-949-016-6832	Sequence 6832, A	_
40	63	76.8	267	2	US-09-949-016-11497	Sequence 11497,	
41	62	75.6	51	1	US-08-346-849-12	Sequence 12, App	
42	62	75.6	51	1	US-08-293-284A-12	Sequence 12, App	
43	62	75.6	51	2	US-08-898-300-12	Sequence 12, App	1
44	62	75.6	51	2	US-08-824-513-12	Sequence 12, App	1
45	62	75.6	199	2	US-09-248-796A-16959	Sequence 16959,	A
46	62	75.6	206	2	US-09-830-230A-294	Sequence 294, Ap	p
47	62	75.6	250	2	US-09-830-230A-293	Sequence 293, Ap	p
48	62	75.6	320	2	US-09-328-352-7937	Sequence 7937, A	-
49	62	75.6	330	1	US-08-868-288A-3	Sequence 3, Appl	-
50	62	75.6	330	2	US-09-235-373-3	Sequence 3, Appl	
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52	62	75.6	330	2	US-09-501-714-3	Sequence 3, Appl	
				2	US-09-248-796A-19195	_	
53	62 63	75.6	347			Sequence 19195,	
54	62 63	75.6	382	2	US-09-603-208A-40	Sequence 40, App	
55	62	75.6	391	2	US-09-902-540-11110	Sequence 11110,	
56	62	75.6	397	2	US-09-248-796A-17628	Sequence 17628,	
57	61	74.4	185	2	US-09-134-000C-6695	Sequence 6695, A	-
58	61	74.4	734	2	US-09-248-796A-16776	Sequence 16776,	
59	60	73.2	75	2	US-09-513-999C-6016	Sequence 6016, A	p.
60	59	72.0	54	1	US-08-346-849-13	Sequence 13, App	1
61	59	72.0	54	1	US-08-293-284A-13	Sequence 13, App	1
62	59	72.0	54	2	US-08-898-300-13	Sequence 13, App	
63	59	72.0	54	2	US-08-824-513-13	Sequence 13, App	
				_		1	-

SCORE Search Results Details for Application 100 and Search Result us-10-001-938-2.rapbm

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2006, 19:29:53; Search time 75.9934 Seconds

(without alignments)

91.432 Million cell updates/sec

Title: US-10-001-938-2

Perfect score: 82

Sequence: 1 RKAYKRLAMKYHPDR 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database: Published_Applications_AA_Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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6: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	82	100.0	15	4	US-10-001-938-2	Sequence 2, Appli
2	82	100.0	52	4	US-10-390-472-8	Sequence 8, Appli
3	82	100.0	376	4	US-10-369-493-689	Sequence 689, App

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                      378
                                                            Sequence 21305, A
        79
                               US-10-369-493-21305
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        75
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                                                            Sequence 386, App
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                                                            Sequence 13658, A
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                                                            Sequence 15487, A
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SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-2.rapbn.

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SCORE **FAQ**

Comments / **Suggestions**

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OM protein - protein search, using sw model

June 2, 2006, 19:30:30; Search time 3.57616 Seconds Run on:

(without alignments)

48.509 Million cell updates/sec

Title: US-10-001-938-2

Perfect score: 82

1 RKAYKRLAMKYHPDR 15 Sequence:

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

58871 seqs, 11565156 residues Searched:

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Published Applications AA New:* Database :

> 1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:*

> 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 NEW PUB.pep:*

4: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

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6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10 NEW PUB.pep:*

7: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11 NEW PUB.pep:*

8: /EMC Celerra SIDS3/ptodata/2/pubpaa/US60 NEW PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

કુ

No.	Score	Match	Length	DB	ID	Description
1	82	100.0	15	6	US-10-490-949-3	Sequence 3, Appli
2	67	81.7	15	6	US-10-490-949-23	Sequence 23, Appl
3	67	81.7	397	7	US-11-293-697-3837	Sequence 3837, Ap
4	65	79.3	95	6	US-10-953-349-31080	Sequence 31080, A
5	65	79.3	156	6	US-10-953-349-5018	Sequence 5018, Ap
6	65	79.3	335	6	US-10-953-349-2182	Sequence 2182, Ap
7	65	79.3	343	6	US-10-953-349-2181	Sequence 2181, Ap
8	63	76.8	349	6	US-10-953-349-948	Sequence 948, App
9	62	75.6	336	6	US-10-953-349-33810	Sequence 33810, A
10	62	75.6	430	6	US-10-953-349-33809	Sequence 33809, A
11	61	74.4	465	6	US-10-953-349-8070	Sequence 8070, Ap
12	61	74.4	473	6	US-10-953-349-8069	Sequence 8069, Ap
13	61	74.4	482	6	US-10-953-349-8068	Sequence 8068, Ap
14	60	73.2	305	6	US-10-953-349-23847	Sequence 23847, A
15	59	72.0	190	6	US-10-953-349-28214	Sequence 28214, A
16	59	72.0	191	6	US-10-953-349-28213	Sequence 28213, A
17	59	72.0	199	6	US-10-953-349-9116	Sequence 9116, Ap
18	59	72.0	248	6	US-10-953-349-9115	Sequence 9115, Ap
19	59	72.0	273	6	US-10-953-349-4464	Sequence 4464, Ap
20	59	72.0	349	6	US-10-953-349-4463	Sequence 4463, Ap
21	59	72.0	367	6	US-10-953-349-4462	Sequence 4462, Ap
22	59	72.0	389	7	US-11-122-986-185	Sequence 185, App
23	59	72.0	389	7	US-11-122-986-187	Sequence 187, App
24	58	70.7	15	6	US-10-490-949-22	Sequence 22, Appl
25	58	70.7	426	7	US-11-293-697-4751	Sequence 4751, Ap
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28	56	68.3	420	6	US-10-953-349-13709	Sequence 13709, A
29	56	68.3	583	6	US-10-953-349-35418	Sequence 35418, A
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34	55	67.1	15	6	US-10-490-949-21	Sequence 21, Appl
35	55	67.1	338	6	US-10-953-349-20361	Sequence 20361, A
36 27	55	67.1	385	6	US-10-953-349-20360	Sequence 20360, A
37 38	55 55	67.1	417	6	US-10-953-349-16377	Sequence 16377, A
30 39	55 55	67.1	419	6	US-10-953-349-1054	Sequence 1054, Ap
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41	53	64.6	110	6	US-10-953-349-54	Sequence 2547, Ap Sequence 54, Appl
42	53	64.6	124	6	US-10-953-349-53	Sequence 54, Appl
43	53	64.6	162	6	US-10-953-349-52	Sequence 52, Appl
44	53	64.6	530	6	US-10-953-349-20585	Sequence 20585, A
45	52	63.4	380	6	US-10-953-349-7175	Sequence 7175, Ap
46	52	63.4	391	6	US-10-953-349-7174	Sequence 7174, Ap
47	52	63.4	442	6	US-10-953-349-7173	Sequence 7173, Ap
48	51	62.2	333	6	US-10-953-349-2863	Sequence 2863, Ap
49	51	62.2	333	6	US-10-953-349-11247	Sequence 11247, A
50	46	56.1	119	6	US-10-953-349-28161	Sequence 28161, A
51	46	56.1	138	6	US-10-953-349-39107	Sequence 39107, A
52	46	56.1	147	6	US-10-953-349-28160	Sequence 28160, A
53	46	56.1	155	6	US-10-953-349-28159	Sequence 28159, A
54	46	56.1	157	6	US-10-953-349-38105	Sequence 38105, A
55	46	56.1	174	6	US-10-953-349-39106	Sequence 39106, A
56	46	56.1	189	7	US-11-293-697-4556	Sequence 4556, Ap
57	46	56.1	192	6	US-10-953-349-38104	Sequence 38104, A
58	46	56.1	367	6	US-10-953-349-1406	Sequence 1406, Ap
59	46	56.1	456	6	US-10-953-349-1405	Sequence 1405, Ap

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-20

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 20.rai.

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:12:07; Search time 12.7 Seconds

(without alignments)

103.383 Million cell updates/sec

Title: US-10-001-938-20

Perfect score: 83

Sequence: 1 SGPFFTFSSSFPGHS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database: Issued Patents AA:*

1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

7: /EMC Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description		
1	83	100.0	277	1	US-08-868-288A-7	Sequence 7, Appli		
2	83	100.0	277	2	US-09-235-373-7	Sequence 7, Appli		

					_		
3	83	100.0	277	2	US-09-388-993-7	_	7, Appli
4	83	100.0	277	2	US-09-501-714-7	•	7, Appli
5	83	100.0	327	2	US-09-949-016-11262	Sequence	11262, A
6	83	100.0	351	1	US-08-868-288A-6	Sequence	6, Appli
7	83	100.0	351	2	US-09-235-373-6	Sequence	6, Appli
8	83	100.0	351	2	US-09-388-993-6	Sequence	6, Appli
9	83	100.0	351	2	US-09-501-714-6	Sequence	6, Appli
10	46	55.4	661	2	US-09-949-016-9121	Sequence	9121, Ap
11	40	48.2	190	2	US-09-270-767-58877	Sequence	58877, A
12	40	48.2	201	1	US-08-155-171B-19	•	19, Appl
13	40	48.2	201	1	US-08-435-998-19	Sequence	
14	40	48.2	204	1	US-08-155-171B-20	Sequence	
15	40	48.2	204	1	US-08-435-998-20	-	20, Appl
16	40	48.2	205	1	US-08-155-171B-17	Sequence	·
17	40	48.2	205	1	US-08-435-998-17	Sequence	
18	40	48.2	206	1	US-08-155-171B-6	•	6, Appli
19	40	48.2	206	1	US-08-435-998-6		6, Appli
		48.2	209	1	US-08-155-171B-18		18, Appl
20	40					•	
21	40	48.2	209	1	US-08-435-998-18	-	18, Appl
22	40	48.2	238	2	US-09-949-016-6334	•	6334, Ap
23	40	48.2	255	2	US-09-949-016-9861	•	9861, Ap
24	40	48.2	280	1	US-08-855-140-1	-	1, Appli
25	40	48.2	286	2	US-09-270-767-43514	_	43514, A
26	40	48.2	297	2	US-10-104-047-2852	-	2852, Ap
27	40	48.2	371	2	US-09-828-302-15	•	15, Appl
28	40	48.2	481	2	US-09-949-016-9509	Sequence	9509, Ap
29	40	48.2	1066	1	US-08-633-770A-1	Sequence	1, Appli
30	40	48.2	1066	2	US-09-280-197-5	Sequence	5, Appli
31	40	48.2	1066	2	US-09-423-126-3	Sequence	3, Appli
32	39	47.0	192	2	US-09-252-991A-32913	Sequence	32913, A
33	39	47.0	236	2	US-08-705-771-19	Sequence	19, Appl
34	39	47.0	236	2	US-09-417-540-19	Sequence	19, Appl
35	39	47.0	259	2	US-09-585-645A-66	Sequence	66, Appl
36	39	47.0	265	1	US-08-807-044-1	Sequence	1, Appli
37	39	47.0	513	2	US-09-862-631-4	Sequence	4, Appli
38	39	47.0	529	2	US-09-801-042-2	Sequence	2, Appli
39	39	47.0	565	2	US-09-489-039A-13730	Sequence	13730, A
40	39	47.0	578	2	US-09-252-991A-16850	Sequence	16850, A
41 .	38.5	46.4	448	2	US-09-198-452A-216	Sequence	216, App
42	38.5	46.4	457	2	US-09-438-185A-199	-	199, App
43	38	45.8	88	2	US-09-513-999C-7631	-	7631, Ap
44	38	45.8	150	2	US-09-540-236-3000	•	3000, Ap
45	38	45.8	319	2	US-09-248-796A-15068	•	15068, A
46	38	45.8	367	2	US-09-949-016-6722	-	6722, Ap
47	38	45.8	405	2	US-09-949-016-9688	•	9688, Ap
48	38	45.8	512	2	US-09-489-039A-10100		10100, A
49	38	45.8	540	2	US-10-094-749-3182	•	3182, Ap
50	38	45.8	548	2	US-09-489-039A-8097	•	8097, Ap
51	37	44.6	33	1	US-08-155-171B-12	•	12, Appl
	37	44.6	33	1	US-08-435-998-12	•	12, Appl
52			61	2	US-09-621-976-5856	•	5856, Ap
53	37	44.6			US-09-621-976-5857	•	5857, Ap
54	37	44.6	61	2		-	-
55 56	37	44.6	61	2	US-09-621-976-5872	•	5872, Ap 3817, Ap
56	37	44.6	105	2	US-10-104-047-3817	-	
57	37	44.6	119	2	US-09-902-540-10567	•	10567, A
58	37	44.6	135	2	US-09-355-040-15	-	15, Appl
59	37	44.6	150	2	US-09-252-991A-24718	•	24718, A
60	37	44.6	203	2	US-09-248-796A-16268	•	16268, A
61	37	44.6	204	1	US-08-155-171B-2	•	2, Appli
62	37	44.6	204	1	US-08-435-998-2	-	2, Appli
63	37	44.6	267	2	US-09-270-767-37278	sequence	37278, A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938 20.rapbm.

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:45:16; Search time 63.4 Seconds

(without alignments)

109.593 Million cell updates/sec

Title: US-10-001-938-20

Perfect score: 83

Sequence: 1 SGPFFTFSSSFPGHS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 1000 summaries

Database: Published Applications AA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query
No. Score Match Length DB ID Description

1 83 100.0 15 4 US-10-001-938-20 Sequence 20, Appl

2	50	60.2	123	3	US-09-925-297-862	Sequence	862, App
3	49	59.0	137	4	US-10-425-115-269076	Sequence	269076,
4	47	56.6	48	4	US-10-425-115-200603	Sequence	·
5	47	56.6	268	4	US-10-282-122A-63570	•	63570, A
				_			·
6	46	55.4	79	4	US-10-425-115-244806	Sequence	244806,
7	46	55.4	625	4	US-10-072-012-699	Sequence	699, App
8	46	55.4	625	5	US-10-029-345A-39	Sequence	39, Appl
9	46	55.4	625	5	US-10-029-345A-110		110, App
				_		_	• • •
10	46	55.4	625	6	US-11-143-984A-39	_	39, Appl
11	46	55.4	625	6	US-11-143-984A-110	Sequence	110, App
12	46	55.4	663	4	US-10-072-012-700	Sequence	700, App
13	46	55.4	663	5	US-10-029-345A-40	Sequence	40, Appl
14	46	55.4	663	6	US-11-143-984A-40	_	40, Appl
						_	
15	45	54.2	129	5	US-10-720-603A-26	•	26, Appl
16	45	54.2	283	4	US-10-437-963-199254	Sequence	199254,
17	44	53.0	115	4	US-10-424-599-152729	Sequence	152729,
18	44	53.0	302	4	US-10-425-114-53866	-	53866, A
19	44	53.0	314	4	US-10-425-115-351784	Sequence	•
						-	•
20	43	51.8	38	4	US-10-437-963-122150	Sequence	· ·
21	43	51.8	53	4	US-10-767-701-62139	Sequence	62139, A
22	43	51.8	93	4	US-10-425-115-317926	Sequence	317926,
23	43	51.8	204	6	US-11-087-099-10169	-	10169, A
	43	51.8		_		•	Ť
24			216	4	US-10-425-114-60968	•	60968, A
25	43	51.8	243	5	US-10-739-930-10203		10203, A
26	43	51.8	261	4	US-10-425-115-262629	Sequence	262629,
27	43	51.8	269	6	US-11-096-568A-15319	Sequence	15319, A
28	43	51.8	283	4	US-10-437-963-126681	Sequence	*
						•	•
29	43	51.8	285	4	US-10-767-701-44420	•	44420, A
30	43	51.8	289	6	US-11-087-099-6104	Sequence	6104, Ap
31	43	51.8	292	6	US-11-087-099-5026	Sequence	5026, Ap
32	43	51.8	292	6	US-11-087-099-12088	Seguence	12088, A
33	43	51.8	292	6	US-11-096-568A-15318	-	15318, A
						•	•
34	43	51.8	294	4	US-10-425-115-262631	Sequence	•
35	43	51.8	351	6	US-11-096-568A-31831	Sequence	31831, A
36	43	51.8	358	6	US-11-096-568A-15317	Sequence	15317, A
37	43	51.8	378	6	US-11-188-298-17261	Seguence	17261, A
38	43	51.8	395	6	US-11-096-568A-31830	•	31830, A
						-	· ·
39	43	51.8	400	6	US-11-096-568A-31829	•	31829, A
40	43	51.8	400	6	US-11-242-650-50	Sequence	50, Appl
41	43	51.8	912	4	US-10-437-963-140140	Sequence	140140,
42	42	50.6	119	4	US-10-425-115-309236	Sequence	309236,
43	42	50.6	127	4	US-10-424-599-269871	Sequence	· · · · · · · · · · · · · · · · · · ·
				-		•	•
44	42	50.6	129	4	US-10-425-115-349086	Sequence	
45	42	50.6	129	5	US-10-720-603A-31		31, Appl
46	42	50.6	145	4	US-10-425-115-276721	Sequence	276721,
47	42	50.6	343	4	US-10-156-761-14087	Sequence	14087, A
48	42	50.6	359	3	US-09-764-864-996	-	996, App
				5		_	
49	42	50.6	402		US-10-719-993-465	_	465, App
50	42	50.6	441	5	US-10-719-993-461	_	461, App
51	42	50.6	441	5	US-10-719-993-463	Sequence	463, App
52	42	50.6	590	5	US-10-719-993-462	Sequence	462, App
53	42	50.6	1020	5	US-10-719-993-464	_	464, App
						•	
54	42	50.6	1229	6	US-11-097-143-42000	•	42000, A
55	41.5	50.0	1010	4	US-10-437-963-180288	Sequence	
56	41	49.4	44	4	US-10-424-599-221131	Sequence	221131,
57	41	49.4	44	4	US-10-425-115-232702	Sequence	232702.
58	41	49.4	65	4	US-10-437-963-148528	Sequence	·
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59	41	49.4	70	4	US-10-424-599-193370	Sequence	
60	41	49.4	76	4	US-10-425-115-186010	Sequence	
61	41	49.4	97	4	US-10-425-115-367760	Sequence	367760,
62	41	49.4	102	4	US-10-425-115-217338	Sequence	217338,
						•	•

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OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:44:08; Search time 3.1 Seconds

(without alignments)

55.960 Million cell updates/sec

Title:

US-10-001-938-20

Perfect score: 83

1 SGPFFTFSSSFPGHS 15 Sequence:

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched:

58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New:*

/EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 NEW_PUB.pep:*

5: /EMC Celerra SIDS3/ptodata/2/pubpaa/PCT NEW PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10 NEW PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /EMC Celerra SIDS3/ptodata/2/pubpaa/US60 NEW PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

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No.	Score	Match	Length	DB	ID	Description
1	83	100.0	15	6	US-10-490-949-29	Sequence 29, Appl
2	43	51.8	265	6	US-10-953-349-11490	Sequence 11490, A
3	43	51.8	309	6	US-10-953-349-11489	Sequence 11489, A
4	43	51.8	314	6	US-10-953-349-11488	Sequence 11488, A
5	43	51.8	400	7	US-11-266-446-50	Sequence 50, Appl
6	40	48.2	236	6	US-10-953-349-7596	Sequence 7596, Ap
7	40	48.2	266	6	US-10-953-349-7595	Sequence 7595, Ap
8	39	47.0	216	6	US-10-953-349-36980	Sequence 36980, A
9	39	47.0	226	6	US-10-953-349-36979	Sequence 36979, A
10	39	47.0	425	6	US-10-953-349-2574	Sequence 2574, Ap
11	38	45.8	404	7	US-11-293-697-4601	Sequence 4601, Ap
12	37	44.6	202	7	US-11-293-697-3481	Sequence 3481, Ap
13	37	44.6	250	6	US-10-953-349-34062	Sequence 34062, A
14	37	44.6	269	6	US-10-953-349-34061	Sequence 34061, A
15	37	44.6	274	6	US-10-953-349-34060	Sequence 34060, A
16	37	44.6	437	7	US-11-293-697-3820	Sequence 3820, Ap
17	37	44.6	641	7	US-11-293-697-3240	Sequence 3240, Ap
18	37	44.6	1336	7	US-11-106-014-92	Sequence 92, Appl
19	36	43.4	192	7	US-11-264-509A-1	Sequence 1, Appli
20	36	43.4	245	6	US-10-953-349-6742	Sequence 6742, Ap
21	36	43.4	259	6	US-10-953-349-6741	Sequence 6741, Ap
22	36	43.4	263	6	US-10-953-349-18437	Sequence 18437, A
23	36	43.4	320	6	US-10-953-349-18436	Sequence 18436, A
24	36	43.4	321	6	US-10-953-349-12608	Sequence 12608, A
25	36	43.4	340	6	US-10-953-349-18435	Sequence 18435, A
26	36	43.4	392	6	US-10-953-349-12607	Sequence 12607, A
27	36	43.4	422	6	US-10-953-349-12606	Sequence 12606, A
28	36	43.4	496	7	US-11-254-252-6	Sequence 6, Appli
29	36	43.4	635	7	US-11-254-252-14	Sequence 14, Appl
30 31	36 36	43.4 43.4	751 3011	7 7	US-11-254-252-12 US-11-140-487A-771	Sequence 12, Appl Sequence 771, App
32	36	43.4	3011	7	US-11-236-836-14	Sequence 14, Appl
33	36	43.4	3011	7	US-11-254-252-20	Sequence 20, Appl
34	35	42.2	100	7	US-11-293-697-2621	Sequence 2621, Ap
35	35	42.2	103	7	US-11-293-697-4841	Sequence 4841, Ap
36	35	42.2		7	US-11-293-697-3004	Sequence 3004, Ap
37	35	42.2	170	6	US-10-953-349-34677	Sequence 34677, A
38	35	42.2	270	6	US-10-953-349-2099	Sequence 2099, Ap
39	35	42.2		6	US-10-953-349-23050	Sequence 23050, A
40	35	42.2	286	6	US-10-953-349-23049	Sequence 23049, A
41	35	42.2	315	6	US-10-953-349-2098	Sequence 2098, Ap
42	35	42.2	334	6	US-10-953-349-23563	Sequence 23563, A
43	35	42.2	337	6	US-10-953-349-2097	Sequence 2097, Ap
44	35	42.2	357	6	US-10-953-349-23048	Sequence 23048, A
45	35	42.2	417	6	US-10-953-349-23562	Sequence 23562, A
46	35	42.2	425	6	US-10-953-349-23561	Sequence 23561, A
47	35	42.2	471	7	US-11-293-697-4551	Sequence 4551, Ap
48	35	42.2	476	6	US-10-505-928-588	Sequence 588, App
49	34	41.0	164	6	US-10-953-349-36053	Sequence 36053, A
50	34	41.0		6	US-10-953-349-37948	Sequence 37948, A
51	34	41.0			US-10-953-349-31456	Sequence 31456, A
52	34	41.0			US-10-953-349-36052	Sequence 36052, A
53	34	41.0		6	US-10-953-349-37947	Sequence 37947, A
54	34	41.0			US-10-953-349-14070	Sequence 14070, A
55	34	41.0			US-10-953-349-14069	Sequence 14069, A
56 53	34	41.0			US-10-953-349-4076	Sequence 4076, Ap
57 50	34	41.0			US-10-953-349-14068	Sequence 14068, A
58 59	34	41.0			US-10-505-928-847 US-10-953-349-4075	Sequence 847, App Sequence 4075, Ap
33	34	41.0	323	6	00.10-300-243-4013	sequence 4013, Ap

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-21.

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OM protein - protein search, using sw model

June 2, 2006, 19:08:52; Search time 11.4238 Seconds Run on:

(without alignments)

114.932 Million cell updates/sec

Title: US-10-001-938-21

Perfect score: 78

1 DGQLKSVTINGVPDD 15 Sequence:

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

650591 seqs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Issued Patents AA:* Database :

> 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/iaa/H_COMB.pep:* 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

/EMC Celerra SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length DB	ID	Description	
1	78	100.0	277 1	US-08-868-288A-7	Sequence 7, Appli	
2	78		277 2	US-09-235-373-7	Sequence 7, Appli	

3	78	100.0	277	2	US-09-388-993-7	Sequence	7, Appli
4	78	100.0	277	2	US-09-501-714-7	Sequence	7, Appli
5	78	100.0	327	2	US-09-949-016-11262	Sequence	11262, A
6	78	100.0	351	1	US-08-868-288A-6	Sequence	6, Appli
7	78	100.0	351	2	US-09-235-373-6	Sequence	6, Appli
8	78	100.0	351	2	US-09-388-993-6	Sequence	6, Appli
9	78	100.0	351	2	US-09-501-714-6	Sequence	6, Appli
10	67	85.9	330	1	US-08-868-288A-3	Sequence	3, Appli
11	67	85.9	330	2	US-09-235-373-3	Sequence	3, Appli
12	67	85.9	330	2	US-09-388-993-3	Sequence	3, Appli
13	67	85.9	330	2	US-09-501-714-3	Sequence	3, Appli
14	44	56.4	1233	2	US-09-134-000C-4971	Sequence	4971, Ap
15	44	56.4	1416	2	US-09-071-035-404	Sequence	404, App
16	44	56.4	1416	2	US-10-206-576-404	Sequence	404, App
17	44	56.4	1448	2	US-09-071-035-402	Sequence	402, App
18	44	56.4	1448	2	US-10-206-576-402	Sequence	402, App
19	42.5	54.5	287	2	US-09-489-039A-10311	Sequence	10311, A
20	40	51.3	333	2	US-09-270-767-46345	•	46345, A
21	40	51.3	497	1	US-09-047-125-3	•	3, Appli
22	40	51.3	497	2	US-07-736-335E-3	-	3, Appli
23	40	51.3	497	2	US-08-709-731A-29	•	29, Appl
24	40	51.3	544	2	US-09-902-540-15796		15796, A
25	40	51.3	873	2	US-09-248-796A-20365	•	20365, A
26	39	50.0	418	2	US-09-843-905A-2		2, Appli
27	39	50.0	418	2	US-09-843-905A-4	•	4, Appli
28	39	50.0	446	2	US-09-252-991A-21834	-	21834, A
29	39	50.0	546	2	US-09-252-991A-22048	•	22048, A
30	39	50.0	636	2	US-09-328-352-5495	-	5495, Ap
31	38	48.7	242	2	US-09-286-690-8	•	8, Appli
32	38	48.7	306	2	US-09-270-767-59593	•	59593, A
33	38	48.7	390	1	US-08-335-583C-2	•	2, Appli
34	38	48.7	503	2	US-09-252-991A-18345	_	18345, A
35	38	48.7	568	2	US-09-248-796A-22993	_	22993, A
36	38	48.7	752	2	US-09-248-796A-15445	•	15445, A
37	38	48.7	768	2	US-09-540-236-3811	_	3811, Ap
38	38	48.7	794	2	US-09-248-796A-18919	•	18919, A
39	38	48.7	887	2	US-10-132-350-18	•	18, Appl
40	38	48.7	887	2	US-10-132-350-20	•	20, Appl
41	38	48.7	991	2	US-09-902-540-11984	-	11984, A
42	38	48.7	1105	2	US-09-270-767-44167	-	44167, A
43	38	48.7	2749	2	US-10-360-101-265	_	265, App
44	37	47.4	221	2	US-09-710-279-2216	_	2216, Ap
45	37	47.4	248	2	US-10-147-874-3	•	3, Appli
46	37	47.4	352	2	US-09-328-352-6547	_	6547, Ap
47	37	47.4	364	2	US-09-489-039A-12541	•	12541, A
48	37	47.4	366	2	US-09-040-681A-6		6, Appli
49	37	47.4	366	2	US-09-497-897-6	•	6, Appli
50	37	47.4	392	2	US-09-013-881-2	•	2, Appli
51	37	47.4	392	2	US-09-612-473-2	•	2, Appli
52	37	47.4	392	2	US-09-724-730-2	•	2, Appli
53	37	47.4	396	2	US-09-252-991A-19425	-	19425, A
54	37	47.4	397	2	US-09-134-001C-5504	•	5504, Ap
55	37	47.4	548	2	US-09-543-681A-6631	•	6631, Ap
56	37	47.4	724	2	US-09-543-681A-4745	•	4745, Ap
5 7	37	47.4	739	2	US-09-248-796A-19328	•	19328, A
5 <i>1</i> 58	37	47.4	754	2	US-09-543-681A-5416		5416, Ap
58 59	37	47.4	975	2	US-09-540-236-2304	•	2304, Ap
60	36	46.2	973 67	2	US-09-540-236-2115	•	2115, Ap
61	36	46.2	119	2	US-09-902-540-10138	•	10138, A
62	36	46.2	158	2	US-09-270-767-31806	•	31806, A
63	36	46.2	197	2	US-09-248-796A-15490	•	15490, A
U.S	30	70.2	191	۷	00 00 240 100M 10490	bequence	10.100/ A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938 21.rapbm.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 21.rapbm.

<u>start</u>

Go Back to pre

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:29:53; Search time 75.9934 Seconds

(without alignments)

91.432 Million cell updates/sec

Title: US-10-001-938-21

Perfect score: 78

Sequence: 1 DGQLKSVTINGVPDD 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 1000 summaries

Database: Published Applications AA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query
No. Score Match Length DB ID Description

1 78 100.0 15 4 US-10-001-938-21 Sequence 21, Appl

2	54	69.2	232	5	US-10-480-988-22	Sequence	22, Appl
3	54	69.2	267	3	US-09-764-868-1164	Sequence	1164, Ap
4	54	69.2	267	3	US-09-764-891-4089	Sequence	4089, Ap
5	52	66.7	242	4	US-10-264-049-2674	Sequence	2674, Ap
6	50	64.1	343	4	US-10-032-201B-274	Sequence	274, App
7	45	57.7	589	4	US-10-260-937-36	Sequence	36, Appl
8	44.5	57.1	745	6	US-11-079-463-6408	Sequence	6408, Ap
9	44	56.4	509	5	US-10-732-923-23606	Sequence	23606, A
10	44	56.4	968	6	US-11-097-143-20043	Sequence	20043, A
11	44	56.4	1416	3	US-09-071-035-404	Sequence	404, App
12	44	56.4	1416	4	US-10-206-576-404	Sequence	404, App
13	44	56.4	1416	5	US-10-912-362-404	Sequence	404, App
14	44	56.4	1448	3	US-09-071-035-402	Sequence	402, App
15	44	56.4	1448	4	US-10-206-576-402	Sequence	402, App
16	44	56.4	1448	5	US-10-912-362-402	Sequence	402, App
17	43	55.1	251	6	US-11-098-686-11007	•	11007, A
18	42	53.8	94	4	US-10-425-115-321280	Sequence	321280,
19	42	53.8	115	4	US-10-425-115-311609	Sequence	· ·
20	42	53.8	525	4	US-10-425-114-44083	Sequence	44083, A
21	42	53.8	620	4	US-10-408-765A-1812	•	1812, Ap
22	42	53.8	692	4	US-10-424-599-150564	Sequence	
23	42	53.8	730	4	US-10-042-865-51	Sequence	51, Appl
24	42	53.8	730	4	US-10-029-020-50	Sequence	50, Appl
25	42	53.8	730	4	US-10-408-765A-2505	-	2505, Ap
26	42	53.8	730	6	US-11-113-424-50	Sequence	50, Appl
27	42	53.8	847	5	US-10-778-804-8	Sequence	8, Appli
28	42	53.8	847	5	US-10-778-804-9	Sequence	9, Appli
29	42	53.8	1086	5	US-10-723-860-3170	Sequence	3170, Ap
30	42	53.8	1086	5	US-10-756-149-5574	•	5574, Ap
31	42	53.8	1688	4	US-10-144-194A-113	Sequence	113, App
32	42	53.8	1688	5	US-10-491-566-113		113, App
33	42	53.8	1688	5	US-10-494-940-52	-	52, Appl
34	42	53.8	1737	3	US-09-808-602-83	· -	83, Appl
35	42	53.8	1737	3	US-09-800-198-71	-	71, Appl
36	42	53.8	2144	5	US-10-723-860-2303	•	2303, Ap
37	42	53.8	2333	5	US-10-453-372-170	_	170, App
38	42	53.8	2551	4	US-10-144-194A-80	-	80, Appl
39	42	53.8	2551	5	US-10-491-566-80	-	80, Appl
40	42	53.8	2633	4	US-10-144-194A-82	-	82, Appl
41	42	53.8	2633	5	US-10-491-566-82	_	82, Appl
42	42	53.8	2662	5	US-10-453-372-114	_	114, App
43	42	53.8	2724	3	US-09-808-602-13	_	13, Appl
44	42	53.8	2724	3	US-09-800-198-13	_	13, Appl
45	42	53.8	2724	5	US-10-453-372-148	_	148, App
46	42	53.8	2733	3	US-09-808-602-8	-	8, Appli
47	42	53.8	2733	3	US-09-800-198-8	_	8, Appli
48	42	53.8	2733	5	US-10-453-372-136	_	136, App
49	42	53.8	2733	5	US-10-453-372-142	_	142, App
50	42	53.8	2733	5	US-10-453-372-146	-	146, App
51	42	53.8	2733	5	US-10-453-372-150	-	150, App
52	42	53.8	2733	5	US-10-453-372-154	-	154, App
53	42	53.8	2758	4	US-10-467-535-10	_	10, Appl
54	42	53.8	2764	3	US-09-808-602-80	-	80, Appl
55 56	42	53.8	2764	3	US-09-800-198-68	-	68, Appl
56 53	42	53.8	2764	4	US-10-072-012-487	—	487, App
57 50	42	53.8	2764	5	US-10-631-467-1514	•	1514, Ap
58 50	42	53.8	2765	3	US-09-808-602-84	_	84, Appl
59 60	42	53.8	2765	3	US-09-800-198-72		72, Appl
60	42	53.8	2765	4	US-10-072-012-488	_	488, App
61 62	42	53.8	2765	5 1	US-10-453-372-116 US-10-383-201-44	_	116, App 44, Appl
62	42	53.8	2769	4	05-10-303-201-44	seduetice	ia' whbi

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-21.rapbn.

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Comments / **Suggestions**

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-001-938-21.rapbn.

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OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:30:30; Search time 3.57616 Seconds

(without alignments)

48.509 Million cell updates/sec

Title:

US-10-001-938-21

Perfect score: 78

1 DGQLKSVTINGVPDD 15

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched:

Sequence:

58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seg length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New: *

/EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11 NEW_PUB.pep:*

/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:* 8:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

No.	Score	Match	Length	DB	ID	Description
1	78	100.0	15	6	US-10-490-949-30	Sequence 30, Appl
2	38	48.7	230	6	US-10-953-349-6513	Sequence 6513, Ap
3	38	48.7	394	6	US-10-953-349-6512	Sequence 6512, Ap
4	37	47.4	216	6	US-10-953-349-5948	Sequence 5948, Ap
5	37	47.4	237	7	US-11-293-697-4647	Sequence 4647, Ap
6	37	47.4	239	6	US-10-953-349-5947	Sequence 5947, Ap
7	36	46.2	301	6	US-10-953-349-18989	Sequence 18989, A
8	36	46.2	351	7	US-11-293-697-2554	Sequence 2554, Ap
9	36	46.2	507	6	US-10-953-349-19123	Sequence 19123, A
10	36	46.2	593	6	US-10-953-349-19122	Sequence 19122, A
11	35.5	45.5	1270	6	US-10-532-050-1	Sequence 1, Appli
12	35.3	44.9	176	6	US-10-953-349-33303	Sequence 33303, A
13	35	44.9	262	6	US-10-953-349-11266	Sequence 11266, A
14	35	44.9	347	6	US-10-953-349-19220	Sequence 19220, A
15	35	44.9	356	6	US-10-953-349-11265	Sequence 11265, A
16		44.9	387	6	US-10-953-349-11264	Sequence 11264, A
	35					Sequence 19219, A
17	35	44.9	465	6	US-10-953-349-19219	_
18	35	44.9	483	6	US-10-953-349-11378	Sequence 11378, A
19	35	44.9	543	7	US-11-293-697-2444	Sequence 2444, Ap
20	34.5	44.2	630	7	US-11-293-697-2818	Sequence 2818, Ap
21	34	43.6		7	US-11-219-563-124	Sequence 124, App
22	34	43.6		6	US-10-953-349-23114	Sequence 23114, A
23	34	43.6		6	US-10-953-349-23113	Sequence 23113, A
24	34	43.6		6	US-10-953-349-25874	Sequence 25874, A
25	34	43.6		6	US-10-953-349-23112	Sequence 23112, A
26	34	43.6		6	US-10-953-349-21574	Sequence 21574, A
27	34	43.6		6	US-10-953-349-28783	Sequence 28783, A
28	34	43.6		6	US-10-953-349-13359	Sequence 13359, A
29	34	43.6		6	US-10-953-349-25873	Sequence 25873, A
30	34	43.6	242	6	US-10-953-349-25872	Sequence 25872, A
31	34	43.6	249	6	US-10-953-349-1158	Sequence 1158, Ap
32	34	43.6	249	6	US-10-953-349-33772	Sequence 33772, A
33	34	43.6	250	6	US-10-953-349-1157	Sequence 1157, Ap
34	34	43.6	255	6	US-10-953-349-19535	Sequence 19535, A
35	34	43.6	279	6	US-10-953-349-13358	Sequence 13358, A
36	34	43.6	286	6	US-10-953-349-13357	Sequence 13357, A
37	34	43.6	299	6	US-10-953-349-19534	Sequence 19534, A
38	34	43.6	306	6	US-10-953-349-19533	Sequence 19533, A
39	34	43.6	316	6	US-10-953-349-21974	Sequence 21974, A
40	34	43.6	364	6	US-10-953-349-22074	Sequence 22074, A
41	34	43.6	370	6	US-10-953-349-21573	Sequence 21573, A
42	34	43.6	371	7	US-11-121-154-174	Sequence 174, App
43	34	43.6	378	6	US-10-953-349-21973	Sequence 21973, A
44	34	43.6	388	6	US-10-953-349-22073	Sequence 22073, A
45	34	43.6	389	6	US-10-953-349-21572	Sequence 21572, A
46	34	43.6		6	US-10-953-349-21972	Sequence 21972, A
47	34	43.6			US-10-953-349-22072	Sequence 22072, A
48	34	43.6			US-10-953-349-9203	Sequence 9203, Ap
49	34	43.6			US-10-953-349-9202	Sequence 9202, Ap
50	34	43.6			US-10-505-928-499	Sequence 499, App
51	33.5	42.9			US-11-313-356-3	Sequence 3, Appli
52	33.3	42.3			US-11-219-563-8	Sequence 8, Appli
53	33	42.3			US-11-219-121-16	Sequence 16, Appl
54	33	42.3			US-10-953-349-40090	Sequence 40090, A
55	33	42.3			US-10-953-349-34327	Sequence 34327, A
56	33	42.3			US-11-106-014-60	Sequence 60, Appl
56 57	33				US-10-511-937-2998	Sequence 2998, Ap
5 <i>1</i> 58		42.3				Sequence 33145, A
58 59	33	42.3			US-10-953-349-35145 US-10-953-349-4567	Sequence 35145, Ap
33	33	42.3	335	0	09-10-303-343-4301	pedaeuce 40011 Wh

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-22.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 22.rai.

start

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OM protein - protein search, using sw model

June 2, 2006, 19:37:25; Search time 14.6053 Seconds Run on:

(without alignments)

89.896 Million cell updates/sec

Title: US-10-001-938-22

Perfect score: 70

Sequence: 1 DLQLAMAYSLSEMEA 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

650591 seqs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Issued Patents AA:* Database :

> /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:* 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:* 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:* /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

/EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Score Match L			ID	Description	
1	70	100.0	277	1	US-08-868-288A-7	Sequence 7, Appli	
2	70	100.0	277	2	US-09-235-373-7	Sequence 7, Appli	

3	70	100.0	277	2	US-09-388-993-7	Sequence	7, Appli
4	70	100.0	277	2	US-09-501-714-7	Sequence	7, Appli
5	70	100.0	327	2	US-09-949-016-11262	Sequence	11262, A
6	70	100.0	351	1	US-08-868-288A-6	Sequence	6, Appli
7	70	100.0	351	2	US-09-235-373-6	Sequence	6, Appli
8	70	100.0	351	2	US-09-388-993-6	•	6, Appli
9	70	100.0	351	2	US-09-501-714-6	•	6, Appli
10	45	64.3	668	2	US-09-538-092-599	_	599, App
		57.1	698	2	US-09-710-279-2388	_	2388, Ap
11	40					•	
12	40	57.1	905	2	US-09-134-001C-3782	•	3782, Ap
13	39	55.7	642	2	US-09-949-016-10283	•	10283, A
14	39	55.7	690	2	US-08-971-089-6	_	6, Appli
15	39	55.7	690	2	US-10-117-604A-6	_	6, Appli
16	39	55.7	776	2	US-09-266-225D-10	-	10, Appl
17	39	55.7	777	2	US-09-949-016-6540	Sequence	6540, Ap
18	38	54.3	472	2	US-08-976-255-17	Sequence	17, Appl
19	36	51.4	164	2	US-09-134-001C-5216	Sequence	5216, Ap
20	36	51.4	425	2	US-09-543-681A-7042	Sequence	7042, Ap
21	36	51.4	508	2	US-10-104-047-2186	•	2186, Ap
22	36	51.4	813	2	US-09-964-899-25	-	25, Appl
23	36	51.4	896	1	US-08-095-737-2	-	2, Appli
		51.4	896	1	US-08-480-145-2	-	2, Appli
24	36			_		-	
25	36	51.4	896	1	US-08-477-389-2	-	2, Appli
26	36	51.4	896	2	US-09-538-092-1113	•	1113, Ap
27	36	51.4	896	2	US-09-949-016-6155	-	6155, Ap
28	36	51.4	897	1	US-08-095-737-4	•	4, Appli
29	36	51.4	897	1	US-08-480-145-4	Sequence	4, Appli
30	36	51.4	897	1	US-08-477-389-4	-	4, Appli
31	36	51.4	926	2	US-09-949-016-10683	Sequence	10683, A
32	35	50.0	119	2	US-09-513-999C-5848	Sequence	5848, Ap
33	35	50.0	155	2	US-09-710-279-344	Sequence	344, App
34	35	50.0	225	2	US-09-543-681A-4987	Sequence	4987, Ap
35	35	50.0	436	2	US-09-902-540-16648	Sequence	16648, A
36	35	50.0	541	2	US-09-252-991A-21132	•	21132, A
37	35	50.0	632	2	US-09-859-961-2	-	2, Appli
38	35	50.0	832	2	US-10-464-939-2	-	2, Appli
39	35	50.0	1058	2	US-10-464-939-4	-	4, Appli
		50.0	1121	2	US-09-949-016-11048	-	11048, A
40	35			_		-	
41	34.5	49.3	486	2	US-09-489-039A-8181	•	8181, Ap
42	34	48.6	98	2	US-09-270-767-57849	-	57849, A
43	34	48.6	131	2	US-09-270-767-31762	-	31762, A
44	34	48.6	131	2	US-09-270-767-46979	_	46979, A
45	34	48.6	218	2	US-09-543-681A-7325	Sequence	-
46	34	48.6	288	2	US-09-134-000C-5520	-	5520, Ap
47	34	48.6	303	2	US-09-252-991A-27331	Sequence	27331, A
48	34	48.6	312	2	US-09-248-796A-16066	Sequence	16066, A
49	34	48.6	334	1	US-08-646-981-16	Sequence	16, Appl
50	34	48.6	351	2	US-09-949-016-8016	Sequence	8016, Ap
51	34	48.6	476	2	US-09-270-767-42546	Sequence	42546, A
52	34	48.6	478	2	US-09-716-964B-142	Sequence	142, App
53	34	48.6	557	2	US-09-248-796A-15455	•	15455, A
54	34	48.6	571	2	US-09-489-039A-14334	-	14334, A
55	34	48.6	601	2	US-09-902-540-11118	•	11118, A
			601	2	US-09-902-540-11118	•	15407, A
56	34	48.6				•	4, Appli
57	34	48.6	716	1	US-08-372-652-4	•	• •
58	34	48.6	716	5	PCT-US95-16311-4	•	4, Appli
59	34	48.6	774	2	US-09-252-991A-29487	-	29487, A
60	34	48.6	923	2	US-09-252-991A-27148	•	27148, A
61	34	48.6	2172	1	US-08-611-107-31	-	31, Appl
62	34	48.6	2257	1	US-08-611-107-10	-	10, Appl
63	34	48.6	2257	1	US-08-422-560A-10	Sequence	10, Appl

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-22.rapbm.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 938-22.rapbm.

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OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:58:51; Search time 63.3553 Seconds

(without alignments)

109.671 Million cell updates/sec

Title:

US-10-001-938-22

Perfect score: 70

1 DLQLAMAYSLSEMEA 15

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched:

Sequence:

2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA Main:*

1: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11 PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No. Score Match Length DB ID

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Description

6/22/06

1	7.0	100 0	1.5	4	110 10 001 039 33		22 71
1	70	100.0	15	4	US-10-001-938-22	_	22, Appl
2	41	58.6	18	3	US-09-971-490-13		13, Appl
3	41	58.6	18	4	US-10-193-452-86	•	86, Appl
4	41	58.6	64	3	US-09-864-761-33889	•	33889, A
5	41	58.6	71	4	US-10-424-599-277428	Sequence	
6	41	58.6	117	4	US-10-108-260A-2985	-	2985, Ap
7	41	58.6	590	4	US-10-275-595A-33	Sequence	33, Appl
8	40	57.1	232	4	US-10-311-035-1	Sequence	1, Appli
9	40	57.1	443	5	US-10-450-763-58647	Sequence	58647, A
10	40	57.1	698	5	US-10-793-626-2388	Sequence	2388, Ap
11	40	57.1	876	3	US-09-815-242-12623	Sequence	12623, A
12	40	57.1	876	4	US-10-282-122A-70369	•	70369, A
13	40	57.1	876	4	US-10-282-122A-70998	•	70998, A
14	40	57.1	876	5	US-10-857-625-697	•	697, App
15	40	57.1	905	4	US-10-724-972A-6007	•	6007, Ap
16	40	57.1	980	3	US-09-888-615-65	•	65, Appl
17		57.1		_	US-10-399-645-6	-	
_	40		980	4		-	6, Appli
18	40	57.1	980	6	US-11-037-243-65	-	65, Appl
19	39	55.7	44	4	US-10-767-701-50107	•	50107, A
20	39	55.7	325	4	US-10-425-115-264787	Sequence	•
21	39	55.7	461	4	US-10-425-115-264789	Sequence	
22	39	55.7	578	4	US-10-425-114-55229	Sequence	55229, A
23	39	55.7	647	6	US-11-097-143-28071	Sequence	28071, A
24	39	55 .7	672	6	US-11-097-143-5211	Sequence	5211, Ap
25	39	55.7	690	4	US-10-117-604-6	Sequence	6, Appli
26	39	55.7	777	4	US-10-257-021-37	Sequence	37, Appl
27	38	54.3	875	4	US-10-282-122A-60678	Sequence	60678, A
28	38	54.3	·875	6	US-11-045-004-1591	•	1591, Ap
29	38	54.3	1413	4	US-10-288-798-24	-	24, Appl
30	38	54.3	1413	4	US-10-362-892-24	-	24, Appl
31	38	54.3	1431	5	US-10-840-512-218	-	218, App
32	38	54.3	1615	4	US-10-343-710-108	-	108, App
					US-10-343-710-100 US-10-369-493-23007	_	23007, A
33	37	52.9	220	4		•	- ·
34	37	52.9	295	4	US-10-437-963-177575	Sequence	
35	37	52.9	704	4	US-10-282-122A-77695	-	77695, A
36	37	52.9	760	4	US-10-437-963-198047	Sequence	· ·
37	37	52.9	813	6	US-11-097-143-40635	-	40635, A
38	36	51.4	164	4	US-10-724-972A-4287	-	4287, Ap
39	36	51.4	170	3	US-09-925-297-575	_	575, App
40	36	51.4	258	5	US-10-739-930-7937	Sequence	7937, Ap
41	36	51.4	308	6	US-11-098-686-11286	Sequence	11286, A
42	36	51.4	321	6	US-11-156-084-168	Sequence	168, App
43	36	51.4	370	4	US-10-425-115-363269	Sequence	363269,
44	36	51.4	380	4	US-10-425-114-67595	Sequence	67595, A
45	36	51.4	448	4	US-10-282-122A-76817	Sequence	76817, A
46	36	51.4	508	4	US-10-104-047-2186	Sequence	2186, Ap
47	36	51.4	508	6	US-11-072-512-2186	•	2186, Ap
48	36	51.4	557	4	US-10-195-962-10	-	10, Appl
49	36	51.4	695	3	US-09-890-688-130	-	130, App
50	36	51.4	813	3	US-09-964-899-25	•	25, Appl
51	36	51.4	813	5	US-10-975-523-25	-	25, Appl
52	36	51.4	824	6	US-11-097-143-10065	-	10065, A
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53 54	36	51.4	824	6	US-11-097-143-10092	•	10092, A
54	36	51.4	952	4	US-10-369-493-5327	•	5327, Ap
55	36	51.4	1101	6	US-11-097-143-9564	•	9564, Ap
56	36	51.4	1369	4	US-10-437-963-184093	Sequence	·
57	36	51.4	1676	4	US-10-128-714-8246	•	8246, Ap
58	36	51.4	1809	5	US-10-745-237-54	-	54, Appl
59	36	51.4	1809	6	US-11-097-143-13683	•	13683, A
60	35	50.0	55	4	US-10-424-599-195544	Sequence	
61	35	50.0	57	4	US-10-425-115-308575	Sequence	308575,

SCORE Search Results Details for Application 10 and Search Result us-10-001-938-22.rapl

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 start

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OM protein - protein search, using sw model

June 2, 2006, 19:45:07; Search time 3.55263 Seconds Run on:

(without alignments)

48.831 Million cell updates/sec

Title: US-10-001-938-22

Perfect score: 70

1 DLQLAMAYSLSEMEA 15 Sequence:

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

58871 seqs, 11565156 residues Searched:

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Published Applications AA New: * Database :

> /EMC Celerra SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:* 2: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 NEW PUB.pep:* 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:* 6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10 NEW PUB.pep:*

> 7: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:* /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description	
1	70	100.0	15	6	US-10-490-949-31	Sequence 31, Appl	
2	41	58.6	117	7	US-11-293-697-2985	Sequence 2985, Ap	

3	38	54.3	1460	7	US-11-247-437-14	Sequence	14, Appl
4	35	50.0	284	6	US-10-953-349-24383	Sequence	24383, A
5	35	50.0	296	6	US-10-953-349-24382	Sequence	24382, A
6	35	50.0	318	6	US-10-953-349-24381	Sequence	24381, A
7	34	48.6	352	7	US-11-293-697-4023	Sequence	4023, Ap
8	34	48.6	468	6	US-10-953-349-3782	-	3782, Ap
9	34	48.6	499	6	US-10-953-349-3781		3781, Ap
10	34	48.6	552	6	US-10-953-349-3780	•	3780, Ap
11		45.7		6	US-10-953-349-9965	-	•
	32		114	-			9965, Ap
12	32	45.7	142	6	US-10-953-349-9964	-	9964, Ap
13	32	45.7	173	7	US-11-297-134-43	_	43, Appl
14	32	45.7	229	1	US-09-725-906B-3	•	3, Appli
15	32	45.7	230	6	US-10-953-349-999	Sequence	999, App
16	32	45.7	338	6	US-10-953-349-2039	Sequence	2039, Ap
17	32	45.7	340	6	US-10-953-349-2038	Sequence	2038, Ap
18	32	45.7	365	6	US-10-953-349-998	Sequence	998, App
19	32	45.7	369	6	US-10-953-349-997	Sequence	997, App
20	32	45.7	414	6	US-10-953-349-4342	-	4342, Ap
21	32	45.7	465	6	US-10-953-349-4341		4341, Ap
22	32	45.7	466	6	US-10-953-349-4340	•	4340, Ap
23	32	45.7	468	6	US-10-953-349-23758	•	23758, A
24	32	45.7	2177	6	US-10-713-648A-64	•	64, Appl
				_		•	• •
25	31	44.3	213	6	US-10-953-349-8603	•	8603, Ap
26	31	44.3	232	6	US-10-953-349-20350	•	20350, A
27	31	44.3	260	6	US-10-953-349-20349	•	20349, A
28	31	44.3	317	6	US-10-953-349-21703	•	21703, A
29	31	44.3	328	6	US-10-953-349-21702	Sequence	21702, A
30	31	44.3	345	6	US-10-953-349-21701	Sequence	21701, A
31	31	44.3	348	6	US-10-953-349-34772	Sequence	34772, A
32	31	44.3	350	6	US-10-953-349-34771	Sequence	34771, A
33	31	44.3	352	6	US-10-953-349-34770	Sequence	34770, A
34	31	44.3	779	6	US-10-531-965-2	-	2, Appli
35	30.5	43.6	1073	6	US-10-713-648A-54	-	54, Appl
36	30	42.9	241	6	US-10-953-349-1750	•	1750, Ap
37	30	42.9	253	6	US-10-953-349-39827	-	39827, A
38	30	42.9	258	6	US-10-953-349-18067	•	18067, A
39	30	42.9	262	6	US-10-953-349-26345	•	26345, A
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40	30	42.9	316	6	US-10-953-349-26344	•	26344, A
41	30	42.9	316	6	US-10-953-349-39826	•	39826, A
42	30	42.9	323	6	US-10-953-349-39825	•	39825, A
43	30	42.9	333	6	US-10-953-349-23660	•	23660, A
44	30	42.9	356	6	US-10-953-349-23659	•	23659, A
45	30	42.9	444	6	US-10-953-349-21229	Sequence	21229, A
46	30	42.9	475	6	US-10-953-349-21228	Sequence	21228, A
47	30	42.9	487	6	US-10-953-349-21227	Sequence	21227, A
48	30	42.9	620	7	US-11-293-697-3458	Sequence	3458, Ap
49	30	42.9	961	6	US-10-548-484-76	Sequence	76, Appl
50	30	42.9	1645	6	US-10-505-928-582	-	582, App
51	29.5	42.1	100	6	US-10-953-349-16837	-	16837, A
52	29.5	42.1	142	6	US-10-953-349-16836	-	16836, A
53	29	41.4	94	6	US-10-953-349-667	•	667, App
54	29	41.4	110	6	US-10-953-349-666	-	666, App
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55	29	41.4	132	6	US-10-953-349-113	_	113, App
56	29	41.4	135	6	US-10-953-349-27142	•	27142, A
57	29	41.4	139	6	US-10-953-349-38612	•	38612, A
58	29	41.4	154	6	US-10-953-349-20540	-	20540, A
59	29	41.4	181	6	US-10-953-349-8622	_	8622, Ap
60	29	41.4	182	6	US-10-953-349-665	Sequence	665, App
61	29	41.4	183	6	US-10-953-349-27141	-	27141, A
62	29	41.4	186	6	US-10-953-349-8621	•	8621, Ap
63	29	41.4	193	6	US-10-953-349-1101		1101, Ap
			-				,

SCORE Search Results Details for Application 10 and Search Result us-10-001-938-23.rai.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 start

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OM protein - protein search, using sw model

June 2, 2006, 19:12:07; Search time 12.7 Seconds Run on:

(without alignments)

103.383 Million cell updates/sec

Title: US-10-001-938-23

Perfect score: 76

Sequence: 1 EDLFMCMDIQLVEAL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Issued Patents AA:* Database :

> /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:* 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:* 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:* 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*

> 6: /EMC Celerra SIDS3/ptodata/2/iaa/RE COMB.pep:* /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description		
1	76	100.0	397	1	US-08-868-288A-5	Sequence 5, Appli		
2	76	100.0	397	2	US-09-235-373-5	Sequence 5, Appli		
3	76	100.0	397	2	US-09-388-993-5	Sequence 5, Appli		

	7.6	100 0	205	_	170	~	450
4	76	100.0	397	2	US-09-919-039-178		178, App
5	76	100.0	397	2	US-09-538-092-1052	_	1052, Ap
6	76	100.0	397	2	US-09-501-714-5	_	5, Appli
7	41	53.9	397	3	US-10-429-223-2	-	2, Appli
8	41	53.9	397	3	US-10-429-223-4	_	4, Appli
9	40	52.6	239	2	US-10-104-047-2162	-	2162, Ap
10	40	52.6	963	1	US-08-537-002A-3	-	3, Appli
11	40	52.6	963	2	US-08-863-010-3	Sequence	3, Appli
12	40	52.6	963	2	US-09-024-429-3	Sequence	3, Appli
13	39	51.3	405	2	US-09-608-285A-25	Sequence	25, Appl
14	39	51.3	405	2	US-09-370-265-25	Sequence	25, Appl
15	39	51.3	405	2	US-09-557-800C-25	Sequence	25, Appl
16	39	51.3	405	2	US-09-370-625A-25	Sequence	25, Appl
17	39	51.3	428	2	US-09-608-285A-3	Sequence	3, Appli
18	39	51.3	428	2	US-09-608-285A-5	Sequence	5, Appli
19	39	51.3	428	2	US-09-608-285A-7	Sequence	7, Appli
20	39	51.3	428	2	US-09-240-639-6	Sequence	6, Appli
21	39	51.3	428	2	US-09-240-639-9	Sequence	9, Appli
22	39	51.3	428	2	US-09-350-836B-3	_	3, Appli
23	39	51.3	428	2	US-09-350-836B-5	_	5, Appli
24	39	51.3	428	2	US-09-350-836B-7	Sequence	
25	39	51.3	428	2	US-09-370-265-3	-	3, Appli
26	39	51.3	428	2	US-09-370-265-5	-	5, Appli
27	39	51.3	428	2	US-09-370-265-7	Sequence	
28	39	51.3	428	2	US-09-557-800C-3	-	3, Appli
29	39	51.3	428	2	US-09-557-800C-5		5, Appli
30	39	51.3	428	2	US-09-557-800C-7	Sequence	
31	39	51.3	428	2	US-09-370-625A-3	_	3, Appli
32	39	51.3	428	2	US-09-370-625A-5	-	5, Appli
33	39	51.3	428	2	US-09-370-625A-7	Sequence	· • •
34	39	51.3	428	2	US-09-908-510A-6	_	
35	39	51.3	428	2	US-09-908-510A-9	-	6, Appli
36	39	51.3	428	2	US-09-905-744B-6	-	9, Appli
37	39	51.3	428	2	US-09-905-744B-9	-	6, Appli
38		51.3				-	9, Appli
	39		428	2	US-10-107-660-6		6, Appli
39	39	51.3	428	2	US-10-107-660-9	Sequence	• •
40	39	51.3	428	2	US-10-107-576-6	_	6, Appli
41	39	51.3	428	2	US-10-107-576-9	-	9, Appli
42	39	51.3	428	2	US-09-905-732B-6	_	6, Appli
43	39	51.3	428	2	US-09-905-732B-9	_	9, Appli
44	39	51.3	428	2	US-09-949-016-6050	_	6050, Ap
45	39	51.3	428	2	US-09-905-743B-6	•	6, Appli
46	39	51.3	428	2	US-09-905-743B-9	•	9, Appli
47	39	51.3	428	2	US-10-091-085-3	_	3, Appli
48	39	51.3	428	2	US-10-091-085-5	Sequence	5, Appli
49	39	51.3	428	2	US-10-091-085-7	Sequence	7, Appli
50	39	51.3	428	2	US-09-905-589-6	Sequence	6, Appli
51	39	51.3	428	2	US-09-905-589-9	Sequence	9, Appli
52	39	51.3	428	2	US-10-108-171A-6	Sequence	6, Appli
53	39	51.3	428	2	US-10-108-171A-9	Sequence	9, Appli
54	39	51.3	470	2	US-09-949-016-11197	Sequence	11197, A
55	38	50.0	148	3	US-09-699-136B-2	Sequence	2, Appli
56	38	50.0	173	2	US-09-270-767-34380	Sequence	34380, A
57	38	50.0	173	2	US-09-270-767-49597	-	49597, A
58	38	50.0	465	2	US-09-240-639-8	-	8, Appli
59	38	50.0	465	2	US-09-557-800C-56		56, Appl
60	38	50.0	465	2	US-09-370-625A-39	-	39, Appl
61	38	50.0	465	2	US-09-908-510A-8	•	8, Appli
62	38	50.0	465	2	US-09-905-744B-8	-	8, Appli
63	38	50.0	465	2	US-10-107-660-8	-	8, Appli
64	38	50.0	465	2	US-10-107-576-8	-	8, Appli
- •				_		2044000	-,

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938 23.rapbm.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 23.rapbm.

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:45:16; Search time 63.4 Seconds

(without alignments)

109.593 Million cell updates/sec

Title: US-10-001-938-23

Perfect score: 76

Sequence: 1 EDLFMCMDIQLVEAL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database: Published Applications AA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		8					
Result No.	Score	Query Match	Length	DB	ID	Description	
1	 76	100.0	 15	4	US-10-001-938-23	Sequence 23, Appl	

2	76	100.0	258	5	US-10-473-127-1141	Sequence	1141, Ap
3	76	100.0	258	5	US-10-473-127-1146	Sequence	1146, Ap
4	76	100.0	397	3	US-09-919-039-178	Sequence	178, App
5	76	100.0	397	5	US-10-473-127-1138	Sequence	1138, Ap
6	76	100.0	397	5	US-10-473-127-1139	Sequence	1139, Ap
7	76	100.0	397	5	US-10-473-127-1140	Sequence	1140, Ap
8	76	100.0	397	5	US-10-473-127-1143	•	1143, Ap
9	76	100.0	397	5	US-10-473-127-1144		1144, Ap
10	76	100.0	397	5	US-10-473-127-1145	-	1145, Ap
11	76	100.0	397	5	US-10-756-149-4727	_	4727, Ap
12	76	100.0	397	5	US-10-631-467-559	-	
				_		-	559, App
13	76 76	100.0	397	5	US-10-631-467-1386	•	1386, Ap
14	76	100.0	397	5	US-10-878-556A-155	-	155, App
15	76	100.0	408	5	US-10-450-763-40099	-	40099, A
16	46	60.5	403	6	US-11-097-143-24405	-	24405, A
17	46	60.5	403	6	US-11-097-143-41904	Sequence	41904, A
18	42	55.3	538	4	US-10-424-599-218710	Sequence	218710,
19	41	53.9	397	4	US-10-429-223-2	Sequence	2, Appli
20	41	53.9	397	4	US-10-429-223-4	Sequence	4, Appli
21	40	52.6	239	4	US-10-104-047-2162	-	2162, Ap
22	40	52.6	239	6	US-11-072-512-2162	-	2162, Ap
23	40	52.6	397	4	US-10-108-260A-3837	-	3837, Ap
24	40	52.6	426	4	US-10-108-260A-4751	-	4751, Ap
25		52.6			US-10-108-200A-4751 US-10-425-115-348539	-	· ·
	40		487	4		Sequence	•
26	40	52.6	524	4	US-10-369-493-6490	•	6490, Ap
27	40	52.6	542	4	US-10-437-963-123435	Sequence	· · · · · · · · · · · · · · · · · · ·
28	39	51.3	194	4	US-10-369-493-17440	-	17440, A
29	39	51.3	330	3	US-09-925-299-876	-	876, App
30	39	51.3	330	3	US-09-925-299-876	Sequence	876, App
31	39	51.3	405	4	US-10-092-063-25	Sequence	25, Appl
32	39	51.3	405	4	US-10-286-926-25	Sequence	25, Appl
33	39	51.3	410	6	US-11-069-543-142	Sequence	142, App
34	39	51.3	428	4	US-10-091-085-3	Sequence	3, Appli
35	39	51.3	428	4	US-10-091-085-5	-	5, Appli
36	39	51.3	428	4	US-10-091-085-7	_	7, Appli
37	39	51.3	428	4	US-10-092-063-3	-	3, Appli
38	39	51.3	428	4	US-10-092-063-5	-	5, Appli
39	39	51.3	428	4	US-10-092-063-7	-	7, Appli
40	39	51.3	428	4	US-10-286-926-3	_	
						-	3, Appli
41	39	51.3	428	4	US-10-286-926-5	-	5, Appli
42	39	51.3	428	4	US-10-286-926-7	-	7, Appli
43	39	51.3	428	4	US-10-231-913-127	-	127, App
44	39	51.3	428	4	US-10-408-765A-2296	•	2296, Ap
45	39	51.3	428	6	US-11-069-543-175		175, App
46	39	51.3	519	4	US-10-408-765A-410	Sequence	410, App
47	38	50.0	39	6	US-11-004-399-286	Sequence	286, App
48	38	50.0	39	6	US-11-004-399-617	Sequence	617, App
49	38	50.0	39	6	US-11-004-399-3928	Sequence	3928, Ap
50	38	50.0	76	4	US-10-425-115-213449	Sequence	213449,
51	38	50.0	119	4	US-10-437-963-163481	Sequence	•
52	38	50.0	148	3	US-09-942-407-2		2, Appli
53	38	50.0	148	4	US-10-371-475-2		2, Appli
54	38	50.0	148	4	US-10-829-897-2	_	2, Appli
55	38	50.0	186	6	US-11-097-143-33963	-	33963, A
56						-	· •
	38	50.0	233	4	US-10-437-963-150553	•	150553,
57 50	38	50.0	407	4	US-10-437-963-150403	-	150403,
58	38	50.0	427	4	US-10-231-913-126	-	126, App
59	38	50.0	465	4	US-10-092-063-39	•	39, Appl
60	38	50.0	537	4	US-10-369-493-8024	→	8024, Ap
61	38	50.0	560	6	US-11-097-143-39837	-	39837, A
62	38	50.0	1080	4	US-10-322-281-626	Sequence	626, App

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-23.rapbn.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:44:08; Search time 3.1 Seconds

(without alignments)

55.960 Million cell updates/sec

Title:

US-10-001-938-23

Perfect score: 76

1 EDLFMCMDIQLVEAL 15 Sequence:

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched:

58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New:*

/EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 NEW PUB.pep:*

4: /EMC_Celerra SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /EMC Celerra SIDS3/ptodata/2/pubpaa/PCT NEW PUB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10 NEW PUB.pep:*

7: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11 NEW PUB.pep:*

/EMC Celerra SIDS3/ptodata/2/pubpaa/US60 NEW PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

No.	Score	Match	Length	DB	ID	Description
1	76	100.0	15	6	US-10-490-949-32	Sequence 32, Appl
2	40	52.6	397	7	US-11-293-697-3837	Sequence 3837, Ap
3	40	52.6	426	7	US-11-293-697-4751	Sequence 4751, Ap
4	36	47.4	257	6	US-10-953-349-1056	Sequence 1056, Ap
5	36	47.4	278	6	US-10-953-349-33998	Sequence 33998, A
6	36	47.4	288	6	US-10-953-349-33997	Sequence 33997, A
7	36	47.4	313	6	US-10-953-349-33996	Sequence 33996, A
8	36	47.4	337	6	US-10-953-349-1055	Sequence 1055, Ap
9	36	47.4	338	6	US-10-953-349-13711	Sequence 13711, A
10	36	47.4	375	6	US-10-953-349-6679	Sequence 6679, Ap
11	36	47.4	382	6	US-10-953-349-13710	Sequence 13710, A
12	36	47.4	419	6	US-10-953-349-1054	Sequence 1054, Ap
13	36	47.4	420	6	US-10-953-349-13709	Sequence 13709, A
14	36	47.4	431	6	US-10-953-349-6678	Sequence 6678, Ap
15	36	47.4	442	6	US-10-953-349-6677	Sequence 6677, Ap
16	35	46.1	842	7	US-11-266-446-68	Sequence 68, Appl
17	34	44.7	191	6	US-10-953-349-12085	Sequence 12085, A
18	34	44.7	358	7	US-11-293-697-2674	Sequence 2674, Ap
19	34	44.7	364	6	US-10-196-749-572	Sequence 572, App
20	34	44.7	621	7	US-11-293-697-4148	Sequence 4148, Ap
21	33.5	44.1	240	6	US-10-953-349-24825	Sequence 24825, A
22	33	43.4	117	6	US-10-953-349-29788	Sequence 29788, A
23	33	43.4	151	6	US-10-953-349-29786	Sequence 29786, A
24	33	43.4	326	7	US-11-140-450-44	Sequence 44, Appl
25	33	43.4	366	7	US-11-255-699-2	Sequence 2, Appli
26	33	43.4	2871	6	US-10-505-928-100	Sequence 100, App
27	32.5	42.8	175	6	US-10-953-349-14897	Sequence 14897, A
28	32.5	42.8	253	6	US-10-953-349-14896	Sequence 14896, A
29	32.5	42.8	296	6	US-10-953-349-14895	Sequence 14895, A
30	32	42.1	147	7	US-11-293-697-2658	Sequence 2658, Ap
31	32	42.1	156	7	US-11-293-697-3460	Sequence 3460, Ap
32	32	42.1	175	7	US-11-075-398-2	Sequence 2, Appli
33	32	42.1	188	6	US-10-953-349-16220	Sequence 16220, A
34	32	42.1	234	6	US-10-953-349-16219	Sequence 16219, A
35	32	42.1	240	6	US-10-953-349-16218	Sequence 16218, A
36 37	32	42.1	286	6	US-10-953-349-30735	Sequence 30735, A
38	32	42.1	304	6	US-10-953-349-30734	Sequence 30734, A
39	32 32	42.1	311 326	6 6	US-10-953-349-16431 US-10-953-349-9889	Sequence 16431, A Sequence 9889, Ap
40	32	42.1	331	6	US-10-953-349-30733	Sequence 30733, A
41	32	42.1	370	6	US-10-953-349-9888	Sequence 9888, Ap
42	32	42.1	380	6	US-10-953-349-20050	Sequence 20050, Ap
43	32	42.1	391	6	US-10-953-349-20049	Sequence 20049, A
44	32	42.1	406	6	US-10-953-349-9887	Sequence 9887, Ap
45	32	42.1	434	6	US-10-953-349-19834	Sequence 19834, A
46	32	42.1	443	6	US-10-953-349-19833	Sequence 19833, A
47	32	42.1	475	6	US-10-953-349-19832	Sequence 19832, A
48	32	42.1	529	6	US-10-953-349-16430	Sequence 16430, A
49	32	42.1	536	6	US-10-953-349-16429	Sequence 16429, A
50	32	42.1	821	6	US-10-505-928-316	Sequence 316, App
51	32	42.1	847	6	US-10-505-928-495	Sequence 495, App
52	31	40.8	226	6	US-10-953-349-35189	Sequence 35189, A
53	31	40.8	244	6	US-10-953-349-26029	Sequence 26029, A
54	31	40.8	254	7	US-11-266-747-1284	Sequence 1284, Ap
55	31	40.8	254	7	US-11-266-747-1710	Sequence 1710, Ap
56	31	40.8	256	6	US-10-953-349-16379	Sequence 16379, A
57	31	40.8	259	6	US-10-953-349-35188	Sequence 35188, A
58	31	40.8	267	6	US-10-953-349-35187	Sequence 35187, A
59	31	40.8	291	6	US-10-953-349-3229	Sequence 3229, Ap

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-24.rai.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-0(938-24.rai.

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OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:12:07; Search time 12.7 Seconds

(without alignments)

103.383 Million cell updates/sec

Title: US-10-001-938-24

Perfect score: 81

Sequence: 1 LCGFQKPISTLDNRT 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 segs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database: Issued Patents AA:*

1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result Query

No. Score Match Length DB ID

Description

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1	81	100.0	397	1	US-08-868-288A-5	Sequence 5, Appli
2	81	100.0	397	2	US-09-235-373-5	Sequence 5, Appli
3	81	100.0	397	2	US-09-388-993-5	Sequence 5, Appli
4	81	100.0	397	2	US-09-919-039-178	Sequence 178, App
5	81	100.0	397	2	US-09-538-092-1052	Sequence 1052, Ap
6	81	100.0	397	2	US-09-501-714-5	Sequence 5, Appli
7	60	74.1	239	2	US-10-104-047-2162	Sequence 2162, Ap
8	55	67.9	397	3	US-10-429-223-2	Sequence 2, Appli
9	55	67.9	397	3	US-10-429-223-4	Sequence 4, Appli
10	53	65.4	347	2	US-09-248-796A-19195	Sequence 19195, A
11	47	58.0	419	1	US-08-686-417-3	Sequence 3, Appli
12	43	53.1	76	2	US-09-252-991A-21761	Sequence 21761, A
13	42	51.9	186	2	US-09-780-016-14	Sequence 14, Appl
14	42	51.9	186	2	US-10-214-811-14	Sequence 14, Appl
15	42	51.9	186	2	US-10-766-074-14	Sequence 14, Appl
16	42	51.9	211	2	US-09-780-016-10	Sequence 10, Appl
17	42	51.9	211	2	US-10-214-811-10	Sequence 10, Appl
18	42	51.9	211	2	US-10-766-074-10	Sequence 10, Appl
19	42	51.9	242	2	US-09-780-016-16	Sequence 16, Appl
20	42	51.9	242	2	US-10-214-811-16	Sequence 16, Appl
21	42	51.9	242	2	US-10-766-074-16	Sequence 16, Appl
22	42	51.9	265	2	US-09-780-016-8	Sequence 8, Appli
23	42	51.9	265	2	US-10-214-811-8	Sequence 8, Appli
24	42	51.9	265	2	US-10-766-074-8	Sequence 8, Appli
25	42	51.9	267	2	US-09-780-016-12	Sequence 12, Appl
26	42	51.9	267	2	US-10-214-811-12	Sequence 12, Appl
27	42	51.9	267	2	US-10-766-074-12	Sequence 12, Appl
28	42	51.9	290	2	US-09-780-016-6	Sequence 6, Appli
29	42	51.9	290	2	US-10-214-811-6	Sequence 6, Appli
30	42	51.9	290	2	US-10-766-074-6	Sequence 6, Appli
31	42	51.9	428	2	US-09-780-016-22	Sequence 22, Appl
32	42	51.9	428	2	US-10-214-811-22	Sequence 22, Appl
33	42	51.9	428	2	US-10-766-074-22	Sequence 22, Appl
34	42	51.9	453	2	US-09-780-016-18	Sequence 18, Appl
35	42	51.9	453	2	US-10-214-811-18	Sequence 18, Appl
36	42	51.9	453	2	US-10-766-074-18	Sequence 18, Appl
37	42	51.9	484	2	US-09-780-016-26	Sequence 26, Appl
38	42	51.9	484	2	US-10-214-811-26	Sequence 26, Appl
39	42	51.9	484	2	US-10-766-074-26	Sequence 26, Appl
40	42	51.9	507	2	US-09-780-016-2	Sequence 2, Appli
41	42	51.9	507	2	US-10-214-811-2	Sequence 2, Appli
42	42	51.9	507	2	US-10-766-074-2	Sequence 2, Appli
43	42	51.9	509	2	US-09-780-016-24	Sequence 24, Appl
44	42	51.9	509	2	US-10-214-811-24	Sequence 24, Appl
45	42	51.9	509	2	US-10-766-074-24	Sequence 24, Appl
46	42	51.9	532	2	US-09-780-016-20	Sequence 20, Appl
47	42	51.9	532	2	US-10-214-811-20	Sequence 20, Appl
48	42	51.9	532	2	US-10-766-074-20	Sequence 20, Appl
49	41	50.6	150	2	US-09-270-767-44364	Sequence 44364, A
50	41	50.6	728	2	US-09-270-767-44662	Sequence 44662, A
51	40	49.4	96	2	US-09-513-999C-6655	Sequence 6655, Ap
52	39.5	48.8	1019	2	US-09-434-066-23	Sequence 23, Appl
53	39	48.1	320	2	US-09-489-039A-10349	Sequence 10349, A
54	39	48.1	340	1	US-08-974-546-5	Sequence 5, Appli
55	39	48.1	340	2	US-09-949-016-6691	Sequence 6691, Ap
56 57	39	48.1	343	2	US-09-328-352-6577	Sequence 6577, Ap
57 50	39	48.1	363	2	US-09-949-016-8899	Sequence 8899, Ap
58 50	38	46.9	100	2	US-08-311-731A-235	Sequence 235, App
59 60	38	46.9	328	2	US-09-328-352-4546	Sequence 4546, Ap
60	38	46.9	336	۷	US-09-270-767-33924	Sequence 33924, A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938 24.rapbm.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 24.rapbm.

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OM protein - protein search, using sw model

June 2, 2006, 19:45:16; Search time 63.4 Seconds Run on:

(without alignments)

109.593 Million cell updates/sec

Title: US-10-001-938-24

Perfect score: 81

1 LCGFQKPISTLDNRT 15 Sequence:

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

2097797 seqs, 463214858 residues Searched:

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA Main:*

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B PUBCOMB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ઠ્ઠ Result Query No. Score Match Length DB ID Description 1 81 100.0 15 4 US-10-001-938-24 Sequence 24, Appl

				_		_	
2	81	100.0	258	5	US-10-473-127-1141	_	1141, Ap
3	81	100.0	258	5	US-10-473-127-1146	_	1146, Ap
4	81	100.0	397	3	US-09-919-039-178	-	178, App
5	81	100.0	397	5	US-10-473-127-1138	•	1138, Ap
6	81	100.0	397	5	US-10-473-127-1140	•	1140, Ap
7	81	100.0	397	5	US-10-473-127-1144	-	1144, Ap
8	81	100.0	397	5	US-10-473-127-1145	•	1145, Ap
9	81	100.0	397	5	US-10-756-149-4727	Sequence	4727, Ap
10	81	100.0	397	5	US-10-631-467-559	Sequence	559, App
11	81	100.0	397	5	US-10-631-467-1386	Sequence	1386, Ap
12	81	100.0	397	5	US-10-878-556A-155	Sequence	155, App
13	81	100.0	408	5	US-10-450-763-40099	Sequence	40099, A
14	76	93.8	397	5	US-10-473-127-1139	Sequence	1139, Ap
15	76	93.8	397	5	US-10-473-127-1143	Sequence	1143, Ap
16	60	74.1	239	4	US-10-104-047-2162	Sequence	2162, Ap
17	60	74.1	239	6	US-11-072-512-2162	Sequence	2162, Ap
18	60	74.1	397	4	US-10-108-260A-3837	Sequence	3837, Ap
19	60	74.1	426	4	US-10-108-260A-4751	Sequence	4751, Ap
20	55	67.9	397	4	US-10-429-223-2	Sequence	2, Appli
21	55	67.9	397	4	US-10-429-223-4	-	4, Appli
22	53	65.4	403	6	US-11-097-143-24405	-	24405, A
23	53	65.4	403	6	US-11-097-143-41904	-	41904, A
24	48	59.3	418	4	US-10-425-115-307678	Sequence	•
25	48	59.3	418	4	US-10-425-115-307679	Sequence	
26	48	59.3	433	4	US-10-425-114-60908	-	60908, A
27	47	58.0	193	4	US-10-425-115-303421	Sequence	•
28	47	58.0	235	6	US-11-096-568A-16063	_	16063, A
29	47	58.0	266	4	US-10-425-115-307674	Sequence	•
30	47	58.0	330	6	US-11-096-568A-16062	•	16062, A
31	47	58.0	336	6	US-11-096-568A-16061	•	16061, A
32	47	58.0	338	6	US-11-096-568A-21865	•	21865, A
33	47	58.0	342	4	US-10-425-114-68558	•	68558, A
34	47	58.0	370	4	US-10-259-194A-44	•	44, Appl
35	47	58.0	417	4	US-10-239-194A-44 US-10-437-963-194306	Sequence	·
36	47	58.0	417	4	US-10-425-115-307680	-	•
36 37	47		417	4		Sequence	
		58.0		4	US-10-437-963-194308	Sequence	•
38	47	58.0	419	-	US-10-767-701-47403	-	47403, A
39	47	58.0	419	4	US-10-425-115-266771	Sequence	•
40	47	58.0	419	4	US-10-425-115-266773	Sequence	·
41	47	58.0	419	4	US-10-425-115-266781	Sequence	•
42	47	58.0	419	4	US-10-425-115-305086	Sequence	Ţ
43	47	58.0	419	6	US-11-096-568A-21864	•	21864, A
44	47	58.0	420	4	US-10-425-115-266776	Sequence	•
45	47	58.0	421	4	US-10-425-114-63525	•	63525, A
46	47	58.0	449	4	US-10-425-114-62758	•	62758, A
47	47	58.0	449	4	US-10-425-114-63503	-	63503, A
48	47	58.0	449	4	US-10-425-114-65975	•	65975, A
49	47	58.0	449	4	US-10-425-114-73027	•	73027, A
50	47	58.0	450	4	US-10-425-114-46482	•	46482, A
51	47	58.0	450	4	US-10-425-114-51073	-	51073, A
52	47	58.0	450	4	US-10-425-114-66222	•	66222, A
53	47	58.0	450	4	US-10-425-114-67773	-	67773, A
54	47	58.0	455	4	US-10-425-114-53631	-	53631, A
55	47	58.0	463	4	US-10-425-114-46997	-	46997, A
56	47	58.0	465	4	US-10-425-114-59416	•	59416, A
57	47	58.0	465	4	US-10-425-114-60884	-	60884, A
58	47	58.0	465	4	US-10-425-114-63473	•	63473, A
59	47	58.0	468	4	US-10-425-114-66072	-	66072, A
60	47	58.0	469	4	US-10-425-114-62592	-	62592, A
61	47	58.0	469	4	US-10-425-114-65844	•	65844, A
62	47	58.0	471	4	US-10-425-114-69286	Sequence	69286, A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-24.rapbn.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-001-938-24.rapbn.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:44:08; Search time 3.1 Seconds

(without alignments)

55.960 Million cell updates/sec

Title:

US-10-001-938-24

Perfect score: 81

Sequence:

1 LCGFQKPISTLDNRT 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched:

58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New: *

/EMC_Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /EMC Celerra SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10 NEW PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11 NEW PUB.pep:*

8: /EMC Celerra SIDS3/ptodata/2/pubpaa/US60 NEW PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

ક્ર

No.	Score	Match	Length	DB	ID	Description
1	81	100.0	15	6	US-10-490-949-33	Sequence 33, Appl
2	60	74.1	397	7	US-11-293-697-3837	Sequence 3837, Ap
3	60	74.1	426	7	US-11-293-697-4751	Sequence 4751, Ap
4	43.5	53.7	792	6	US-10-953-349-38485	Sequence 38485, A
5	43.5	53.7	805	6	US-10-953-349-38484	Sequence 38484, A
6	43.5	53.7	857	6	US-10-953-349-38483	Sequence 38483, A
7	42	51.9	256	6	US-10-953-349-16379	Sequence 16379, A
8	42	51.9	336	6	US-10-953-349-16378	Sequence 16378, A
9	42	51.9	338	6	US-10-953-349-13711	Sequence 13711, A
10	42	51.9	382	6	US-10-953-349-13710	Sequence 13710, A
11	42	51.9	417	6	US-10-953-349-16377	Sequence 16377, A
12	42	51.9	420	6	US-10-953-349-13709	Sequence 13709, A
13	41	50.6	257	6	US-10-953-349-1056	Sequence 1056, Ap
14	41	50.6	337	6	US-10-953-349-1055	Sequence 1055, Ap
15	41	50.6	419	6	US-10-953-349-1054	Sequence 1054, Ap
16	41	50.6	487	6	US-10-953-349-953	Sequence 953, App
17	41	50.6	546	6	US-10-953-349-952	Sequence 952, App
18	39	48.1	189	6	US-10-953-349-29757	Sequence 29757, A
19	39	48.1	210	6	US-10-953-349-29756	Sequence 29756, A
20	39	48.1	241	6	US-10-953-349-29755	Sequence 29755, A
21	38	46.9	307	6	US-10-953-349-2183	Sequence 2183, Ap
22	38	46.9	335	6	US-10-953-349-2182	Sequence 2182, Ap
23	38	46.9	343	6	US-10-953-349-2181	Sequence 2181, Ap
24	35	43.2	109	6	US-10-953-349-13281	Sequence 13281, A
25	35	43.2	121	6	US-10-953-349-13280	Sequence 13280, A
26	35	43.2	131	6	US-10-953-349-13279	Sequence 13279, A
27	35	43.2	139	6	US-10-953-349-12099	Sequence 12099, A
28	35	43.2	153	7	US-11-293-697-3623	Sequence 3623, Ap
29	35	43.2	155	6	US-10-953-349-12098	Sequence 12098, A
30	35	43.2	256	6	US-10-953-349-12097	Sequence 12097, A
31	35	43.2	357	6	US-10-953-349-19869	Sequence 19869, A
32	35	43.2	380	6	US-10-953-349-19868	Sequence 19868, A
33	35	43.2	388	6	US-10-953-349-19867	Sequence 19867, A
34	35	43.2	786	7	US-11-177-635-8	Sequence 8, Appli
35	34	42.0	168	6	US-10-953-349-18747	Sequence 18747, A
36	34	42.0	171	6	US-10-953-349-18746	Sequence 18746, A
37	34	42.0	211	6	US-10-953-349-18745	Sequence 18745, A
38	34	42.0	336	6	US-10-953-349-5628	Sequence 5628, Ap
39	34	42.0	383	6	US-10-953-349-18444	Sequence 18444, A
40	34	42.0	400	6	US-10-953-349-18443	Sequence 18443, A
41	34	42.0	483	6	US-10-953-349-11378	Sequence 11378, A
42 43	34 34	42.0	512	7	US-11-293-697-4080	Sequence 4080, Ap
43		42.0	523	6	US-10-953-349-20058	Sequence 20058, A
45	34	42.0	545	6	US-10-953-349-20057	Sequence 20057, A
	34	42.0	557	6	US-10-953-349-20056	Sequence 20056, A
46 47	33.5 33.5	41.4 41.4	211 377	6	US-10-953-349-12022	Sequence 12022, A
48		40.7	126	6 6	US-10-953-349-12021 US-10-953-349-15907	Sequence 12021, A
49	33	40.7	158		US-10-953-349-9661	Sequence 15907, A
50	33 33	40.7	160	6 6	US-10-953-349-28747	Sequence 9661, Ap
51	33	40.7	162	6	US-10-953-349-28747	Sequence 28747, A Sequence 15906, A
52	33	40.7	168	6	US-10-953-349-15906 US-10-953-349-9660	Sequence 15906, Ap
53	33	40.7	170	6	US-10-953-349-15905	Sequence 15905, Ap
53 54	33	40.7	184	6	US-10-953-349-15905 US-10-953-349-28745	Sequence 15905, A Sequence 28745, A
55 55	33	40.7	221	6	US-10-953-349-28745	Sequence 28745, A Sequence 11731, A
56	33	40.7	222	6	US-10-953-349-11731	Sequence 11731, A Sequence 11730, A
57	33	40.7	226		· US-10-505-928-193	Sequence 11730, A Sequence 193, App
58	33	40.7	308	6	US-10-953-349-33811	Sequence 33811, A
59	33	40.7	317	6	US-10-953-349-11729	Sequence 11729, A
		10.7	J = 1	-		20420100 11,201 R

SCORE Search Results Details for Application 100 and Search Result us-10-001-938-25.rai.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 25.rai.

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:37:25; Search time 14.6053 Seconds

(without alignments)

89.896 Million cell updates/sec

Title: US-10-001-938-25

Perfect score: 78

Sequence: 1 RTIVITSHPGQIVKH 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database: Issued Patents AA:*

1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	78	100.0	397	1	US-08-868-288A-5	Sequence 5, Appli
2	78	100.0	397	2	US-09-235-373-5	Sequence 5, Appli

_				_			
3	78	100.0	397	2	US-09-388-993-5	•	5, Appli
4	78	100.0	397	2	US-09-919-039-178	-	178, App
5	78	100.0	397	2	US-09-538-092-1052	_	1052, Ap
6	78	100.0	397	2	US-09-501-714-5	_	5, Appli
7	49	62.8	397	3	US-10-429-223-2	Sequence	2, Appli
8	49	62.8	397	3	US-10-429-223-4	Sequence	4, Appli
9	48	61.5	239	2	US-10-104-047-2162	Sequence	2162, Ap
10	44	56.4	26	2	US-10-057-789-126	Sequence	126, App
11	44	56.4	27	2	US-10-057-789-128	Sequence	128, App
12	43	55.1	198	2	US-09-270-767-41637	Sequence	41637, A
13	42	53.8	155	2	US-09-087-134-12	Sequence	12, Appl
14	42	53.8	228	2	US-09-949-002-409	Sequence	409, App
15	42	53.8	267	2	US-09-328-352-6820	•	6820, Ap
16	42	53.8	518	2	US-09-113-309-19	-	19, Appl
17	42	53.8	518	2	US-09-521-109-19	-	19, Appl
18	42	53.8	518	2	US-09-562-332-19	-	19, Appl
19	42	53.8	534	2	US-09-087-134-11	_	11, Appl
20	42	53.8	824	2	US-09-949-002-312		312, App
21	41	52.6	43	2	US-09-270-767-61905	_	61905, A
22	41	52.6	326	2	US-09-270-767-46335	-	•
				2		-	46335, A
23	41	52.6	522		US-09-489-039A-10041	•	10041, A
24	40	51.3	266	2	US-09-949-016-8843	-	8843, Ap
25	40	51.3	266	2	US-09-949-016-8844	-	8844, Ap
26	40	51.3	397	1	US-08-371-377-19	-	19, Appl
27	40	51.3	397	2	US-08-875-553D-25	Sequence	• •
28	40	51.3	398	1	US-08-371-377-17	_	17, Appl
29	40	51.3	398	2	US-08-875-553D-23	_	23, Appl
30	40	51.3	419	1	US-08-686-417-3	Sequence	3, Appli
31	40	51.3	462	1	US-08-299-351-1	Sequence	1, Appli
32	40	51.3	462	1	US-08-371-377-18	Sequence	18, Appl
33	40	51.3	462	2	US-09-309-572-10	Sequence	10, Appl
34	40	51.3	462	2	US-09-718-096-10	Sequence	10, Appl
35	40	51.3	462	2	US-08-875-553D-24	Sequence	24, Appl
36	40	51.3	462	2	US-09-949-016-6075	Sequence	6075, Ap
37	40	51.3	462	7	5225348-1	Patent No	. 5225348
38	40	51.3	469	2	US-09-949-016-7704	Sequence	7704, Ap
39	40	51.3	469	2	US-09-949-016-9570	Sequence	9570, Ap
40	40	51.3	469	2	US-09-949-016-9571	-	9571, Ap
41	40	51.3	478	2	US-09-949-016-7819	•	7819, Ap
42	40	51.3	510	2	US-09-252-991A-33009	•	33009, A
43	39	50.0	128	2	US-09-270-767-42059	•	42059, A
44	39	50.0	460	2	US-09-174-768-4	-	4, Appli
45	39	50.0	460	2	US-09-248-796A-19819	-	19819, A
46	39	50.0	528	2	US-09-252-991A-22551	•	22551, A
47	39	50.0	1159	1	US-08-956-242-13	•	13, Appl
48	39	50.0	1159	2	US-09-351-215-13		13, Appl
49	39	50.0	1159	2	US-09-226-012-2	•	2, Appli
50	39	50.0	1159	2	US-09-226-012-4	-	4, Appli
51	39	50.0	1159	2	US-09-358-383C-10	_	10, Appl
52	39	50.0	1159	2	US-09-275-252A-12	_	12, Appl
53	38.5	49.4	576	2	US-09-328-352-7413	_	7413, Ap
54	38	48.7	70	2	US-09-107-433-4651	•	4651, Ap
				_		•	•
55 56	38 38	48.7 48.7	151 326	2	US-09-583-110-3331 US-09-134-000C-5365	•	3331, Ap 5365, Ap
				_		-	•
57	38	48.7	420	2	US-09-213-053-4	•	4, Appli
58	38	48.7	426	2	US-09-248-796A-15263	-	15263, A
59	38	48.7	485	2	US-09-252-991A-31157	-	31157, A
60	38	48.7	511	2	US-09-902-540-10893	-	10893, A
61	38	48.7	889	2	US-09-902-540-15702	•	15702, A
62	38	48.7	1060	2	US-09-248-796A-18062	•	18062, A
63	38	48.7	1394	2	US-09-213-053-2	Sequence	2, Appli

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938 25.rapbm.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-0(25.rapbm.

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:58:51; Search time 63.3553 Seconds

(without alignments)

109.671 Million cell updates/sec

Title: US-10-001-938-25

Perfect score: 78

Sequence: 1 RTIVITSHPGQIVKH 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 1000 summaries

Database: Published Applications AA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length 1	DB	ID	Description		
1	78	100.0	15	4	US-10-001-938-25	Sequence 25, Appl		

		100 0	0.5.0	_			
2	78	100.0	258	5	US-10-473-127-1141	Sequence	1141, Ap
3	78	100.0	258	5	US-10-473-127-1146	Sequence	1146, Ap
4	78	100.0	397	3	US-09-919-039-178	Sequence	178, App
5	78	100.0	397	5	US-10-473-127-1138	Sequence	1138, Ap
6	78	100.0	397	5	US-10-473-127-1139	Sequence	1139, Ap
7	78	100.0	397	5	US-10-473-127-1140	Sequence	1140, Ap
8	78	100.0	397	5	US-10-473-127-1143	Sequence	1143, Ap
9	78	100.0	397	5	US-10-473-127-1144	Sequence	1144, Ap
10	78	100.0	397	5	US-10-473-127-1145	•	1145, Ap
11	78	100.0	397	5	US-10-756-149-4727	•	4727, Ap
12	78	100.0	397	5	US-10-631-467-559	•	559, App
13	78	100.0	397	5	US-10-631-467-1386	-	1386, Ap
14	78	100.0	397	5	US-10-878-556A-155	•	155, App
15	78	100.0	408	5	US-10-450-763-40099	-	40099, A
16	49	62.8	397	4	US-10-429-223-2	-	·
17		62.8		-		-	2, Appli
	49		397	4	US-10-429-223-4		4, Appli
18	49	62.8	1034	4	US-10-369-493-2756	•	2756, Ap
19	48	61.5	239	4	US-10-104-047-2162	-	2162, Ap
20	48	61.5	239	6	US-11-072-512-2162	Sequence	· -
21	48	61.5	397	4	US-10-108-260A-3837	Sequence	3837, Ap
22	48	61.5	426	4	US-10-108-260A-4751	Sequence	4751, Ap
23	45	57.7	403	6	US-11-097-143-24405	Sequence	24405, A
24	45	57.7	403	6	US-11-097-143-41904	Sequence	41904, A
25	45	57.7	973	4	US-10-369-493-21064	Sequence	21064, A
26	45	57.7	982	4	US-10-369-493-18879	Sequence	18879, A
27	45	57.7	993	4	US-10-369-493-20014	•	20014, A
28	44	56.4	26	4	US-10-057-789-126	•	126, App
29	44	56.4	26	4	US-10-212-628-126	—	126, App
30	44	56.4	27	4	US-10-057-789-128	-	128, App
31	44	56.4	27	4	US-10-212-628-128	-	128, App
32	44	56.4	458	4	US-10-369-493-1461	-	1461, Ap
33	44	56.4	458	4	US-10-369-493-22525	-	22525, A
34	44	56.4	458	5	US-10-303-433-22323 US-10-494-175-23	•	•
35	43	55.1	375	5	US-10-732-923-17660	-	23, Appl
36	43	55.1	375	5		-	17660, A
37				_	US-10-732-923-17665	-	17665, A
	43	55.1	764	4	US-10-166-087-16	•	16, Appl
38	43	55.1	1693	4	US-10-437-963-189648	Sequence	•
39	42	53.8	129	4	US-10-425-115-307676	Sequence	•
40	42	53.8	136	4	US-10-767-701-47402	•	47402, A
41	42	53.8	155	4	US-10-044-442-12	_	12, Appl
42	42	53.8	235	6	US-11-096-568A-16063	Sequence	16063, A
43	42	53.8	246	4	US-10-424-599-258384	Sequence	258384,
44	42	53.8	266	4	US-10-425-115-307674	Sequence	307674,
45	42	53.8	306	4	US-10-425-114-51732	Sequence	51732, A
46	42	53.8	330	6	US-11-096-568A-16062	Sequence	16062, A
47	42	53.8	336	6	US-11-096-568A-16061	Sequence	16061, A
48	42	53.8	342	4	US-10-425-114-68558	Sequence	68558, A
49	42	53.8	363	4	US-10-425-115-304214	Sequence	304214,
50	42	53.8	402	4	US-10-343-953-2	Sequence	2, Appli
51	42	53.8	402	4	US-10-257-174-47	-	47, Appl
52	42	53.8	402	5	US-10-481-698-17	-	17, Appl
53	42	53.8	402	6	US-11-174-150-47	-	47, Appl
54	42	53.8	408	5	US-10-732-923-17717	-	17717, A
55	42	53.8	409	5	US-10-732-923-17539	-	17539, A
56	42	53.8	409	5	US-10-732-923-17544	-	17544, A
57	42	53.8	410	4	US-10-424-599-271035	Sequence	· ·
58	42	53.8	410	5	US-10-204-639-43	-	43, Appl
59	42	53.8	417	4	US-10-204-639-43 US-10-424-599-186616	•	` - -
60	42					Sequence	•
		53.8	417	4	US-10-424-599-271037	Sequence	
61 62	42	53.8	417	4	US-10-425-115-307680	Sequence	
62	42	53.8	418	4	US-10-425-115-307678	Sequence	30/6/8,

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-25.rapbn.

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Comments / **Suggestions**

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 938-25.rapbn.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:45:07; Search time 3.55263 Seconds

(without alignments)

48.831 Million cell updates/sec

Title:

US-10-001-938-25

Perfect score: 78

1 RTIVITSHPGQIVKH 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

Sequence:

58871 segs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seg length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New: *

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /EMC Celerra SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

7: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11 NEW PUB.pep:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

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No.	Score	Match	Length	DB	ID	Description
1	78	100.0	15	6	US-10-490-949-34	Sequence 34, Appl
2	48	61.5	397	7	US-11-293-697-3837	Sequence 3837, Ap
3	48	61.5	426	7	US-11-293-697-4751	Sequence 4751, Ap
4	42	53.8	256	6	US-10-953-349-16379	Sequence 16379, A
5	42	53.8	336	6	US-10-953-349-16378	Sequence 16378, A
6	42	53.8	417	6	US-10-953-349-16377	Sequence 16377, A
7	41	52.6	338	6	US-10-953-349-13711	Sequence 13711, A
8	41	52.6	382	6	US-10-953-349-13710	Sequence 13710, A
9	41	52.6	420	6	US-10-953-349-13709	Sequence 13709, A
10	40	51.3	257	6	US-10-953-349-1056	Sequence 1056, Ap
11	40	51.3	268	6	US-10-953-349-21449	Sequence 21449, A
12	40	51.3	300	6	US-10-953-349-21447	Sequence 21447, A
13	40	51.3	337	6	US-10-953-349-1055	Sequence 1055, Ap
14	40	51.3	346	6	US-10-953-349-23983	Sequence 23983, A
15	40	51.3	348	6	US-10-953-349-7255	Sequence 7255, Ap
16	40	51.3	348	6	US-10-953-349-38793	Sequence 38793, A
17	40	51.3	399	6	US-10-953-349-23982	Sequence 23982, A
18	40	51.3	399	6	US-10-953-349-35097	Sequence 35097, A
19	40	51.3	401	6	US-10-953-349-7254	Sequence 7254, Ap
20	40	51.3	401	6	US-10-953-349-38792	Sequence 38792, A
21	40	51.3	419	6	US-10-953-349-1054	Sequence 1054, Ap
22	40	51.3	447	6	US-10-953-349-23981	Sequence 23981, A
23	40	51.3	447	6	US-10-953-349-35096	Sequence 35096, A
24	40	51.3	449	6	US-10-953-349-7253	Sequence 7253, Ap
25	40	51.3	449	6	US-10-953-349-38791	Sequence 38791, A
26	40	51.3	462	6	US-10-511-937-2558	Sequence 2558, Ap
27	40	51.3	463	6	US-10-516-478-6	Sequence 6, Appli
28	40	51.3	485	6	US-10-953-349-35095	Sequence 35095, A
29	38	48.7	681	7	US-11-293-697-3408	Sequence 3408, Ap
30 31	38 37	48.7 47.4	681 210	7	US-11-293-697-3639	Sequence 3639, Ap
32	37	47.4	288	6 6	US-10-953-349-31668 US-10-953-349-31667	Sequence 31668, A
33	37	47.4	306	6	US-10-953-349-31666	Sequence 31667, A Sequence 31666, A
34	37	47.4	1395	6	US-10-505-928-513	Sequence 513, App
35	36	46.2	252	6	US-10-953-349-20106	Sequence 20106, A
36	36	46.2	263	6	US-10-953-349-20105	Sequence 20105, A
37	36	46.2	304	6	US-10-953-349-20104	Sequence 20104, A
38	36	46.2	426	6	US-10-953-349-2596	Sequence 2596, Ap
39	36	46.2	649	6	US-10-953-349-2595	Sequence 2595, Ap
40	36	46.2	667	6	US-10-953-349-2594	Sequence 2594, Ap
41	35	44.9	144	6	US-10-953-349-2402	Sequence 2402, Ap
42	35	44.9	197	6	US-10-953-349-13929	Sequence 13929, A
43	35	44.9	200	6	US-10-953-349-2401	Sequence 2401, Ap
44	35	44.9	208	6	US-10-953-349-2400	Sequence 2400, Ap
45	35	44.9	331	6	US-10-196-749-162	Sequence 162, App
46	35	44.9	331	7	US-11-101-316-36	Sequence 36, Appl
47	35	44.9	331	7	US-11-305-413-12	Sequence 12, Appl
48	35	44.9	434	7	US-11-106-014-24	Sequence 24, Appl
49	35	44.9	883	7	US-11-297-383-11	Sequence 11, Appl
50	34	43.6	87	6	US-10-953-349-37142	Sequence 37142, A
51	34	43.6	125	7	US-11-293-697-4630	Sequence 4630, Ap
52	34	43.6	128	6	US-10-953-349-2235	Sequence 2235, Ap
53	34	43.6	163	7	US-11-249-111-107	Sequence 107, App
54	34	43.6	194	6	US-10-510-162-4	Sequence 4, Appli
55	34	43.6	195	6	US-10-953-349-2234	Sequence 2234, Ap
56	34	43.6	195	6	US-10-953-349-37209	Sequence 37209, A
57	34	43.6	198	6	US-10-953-349-2233	Sequence 2233, Ap
58	34	43.6	198	6	US-10-953-349-37208	Sequence 37208, A
59	34	43.6	214	6	US-10-953-349-37207	Sequence 37207, A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-26

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 26.rai.

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:08:52; Search time 11.4238 Seconds

(without alignments)

114.932 Million cell updates/sec

Title: US-10-001-938-26

Perfect score: 79

Sequence: 1 GRLIIEFKVNFPENG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database: Issued Patents AA:*

1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length DB ID			Description
1	79	100.0		1	US-08-868-288A-5	Sequence 5, Appli
2	79	100.0	397	2	US-09-235-373-5	Sequence 5, Appli

_				_			
3	79	100.0	397	2	US-09-388-993-5	-	5, Appli
4	79	100.0	397	2	US-09-919-039-178	Sequence	178, App
5	79	100.0	397	2	US-09-538-092-1052	Sequence	1052, Ap
6	79	100.0	397	2	US-09-501-714-5	Sequence	5, Appli
7	52	65.8	397	2	US-09-248-796A-17628	Sequence	17628, A
8	50	63.3	348	1	US-08-974-546-1	Sequence	1, Appli
9	47	59.5	340	1	US-08-974-546-5	_	5, Appli
10	47	59.5	340	2	US-09-949-016-6691	•	6691, Ap
11	47	59.5	363	2	US-09-949-016-8899	•	8899, Ap
12				3	US-10-429-223-3	•	· -
	46	58.2	334				3, Appli
13	46	58.2	337	2	US-09-665-479A-8		8, Appli
14	45	57.0	77	2	US-09-270-767-57315	•	57315, A
15	45	57.0	128	2	US-09-270-767-42059	Sequence	42059, A
16	43	54.4	666	2	US-09-134-001C-5465	Sequence	5465, Ap
17	42	53.2	86	1	US-08-785-795-1	Sequence	1, Appli
18	42	53.2	397	3	US-10-429-223-2	Sequence	2, Appli
19	41	51.9	96	2	US-09-248-796A-21503	-	21503, A
20	41	51.9	662	2	US-09-583-110-4571	<u>-</u>	4571, Ap
21	41	51.9	679	2	US-09-107-433-3402	-	3402, Ap
22	40.5	51.3	74	2	US-09-270-767-57464	•	57464, A
				_		•	-
23	40.5	51.3	262	2	US-09-270-767-42193	_	42193, A
24	40	50.6	239	2	US-10-104-047-2162	•	2162, Ap
25	40	50.6	358	1	US-08-868-288A-1	-	1, Appli
26	40	50.6	358	2	US-09-235-373-1	Sequence	1, Appli
27	40	50.6	358	2	US-09-388-993-1	Sequence	1, Appli
28	40	50.6	358	2	US-09-991-181-148	Sequence	148, App
29	40	50.6	358	2	US-09-501-714-1	Sequence	1, Appli
30	40	50.6	358	2	US-09-990-444-148	_	148, App
31	40	50.6	358	2	US-09-997-333-148	_	148, App
32	40	50.6	358	2	US-09-992-598-148	-	148, App
33	40	50.6	358	2	US-09-989-735-148	Sequence	
						•	· _
34	40	50.6	358	3	US-09-989-726-148	Sequence	
35	40	50.6	358	3	US-09-997-514-148	Sequence	, -
36	40	50.6	358	3	US-09-989-728-148	_	148, App
37	40	50.6	358	3	US-09-997-349-148	-	148, App
38	40	50.6	358	3	US-09-997-653-148	-	148, App
39	40	50.6	358	3	US-09-989-293A-148	Sequence	148, App
40	40	50.6	419	1	US-08-686-417-3	Sequence	3, Appli
41	40	50.6	428	1	US-08-889-711-4	Sequence	4, Appli
42	40	50.6	428	2	US-09-185-825-4	-	4, Appli
43	40	50.6	763	1	US-08-889-711-2	-	2, Appli
44	40	50.6	763	2	US-09-185-825-2	_	2, Appli
45	40	50.6	763	2	US-09-583-110-3773	_	3773, Ap
46	40	50.6	776	2	US-09-107-433-3635	-	3635, Ap
				_		-	
47	39		312	2	US-09-538-092-256	-	256, App
48	39	49.4	319	2	US-09-248-796A-18323	•	18323, A
49	39	49.4	323	2	US-09-538-092-1093	-	1093, Ap
50	39	49.4	327	2	US-09-538-092-1095		1095, Ap
51	39	49.4	327	2	US-09-949-016-6266	Sequence	6266, Ap
52	39	49.4	330	2	US-09-167-206-6	Sequence	6, Appli
53	39	49.4	330	2	US-09-538-092-873	Sequence	873, App
54	39	49.4	330	2	US-09-190-976B-8	Sequence	8, Appli
55	39	49.4	356	2	US-09-949-016-8084		8084, Ap
56	39	49.4	374	2	US-09-949-016-7363	-	7363, Ap
57	39	49.4	431	2	US-09-248-796A-16312	•	16312, A
5 <i>1</i>	39	49.4	685	2	US-10-094-749-2360	•	2360, Ap
				_		•	•
59	38	48.1	49	2	US-09-270-767-33329	•	33329, A
60	38	48.1	49	2	US-09-270-767-48546	•	48546, A
61	38	48.1	78	1	US-08-117-952-752	-	752, App
62	38	48.1	106	2	US-09-746-801A-49	_	49, Appl
63	38	48.1	106	2	US-10-719-885-49	Sequence	49, Appl

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938 26.rapbm.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 26.rapbm.

start

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

June 2, 2006, 19:29:53; Search time 75.9934 Seconds Run on:

(without alignments)

91.432 Million cell updates/sec

Title: US-10-001-938-26

Perfect score: 79

1 GRLIIEFKVNFPENG 15 Sequence:

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

2097797 seqs, 463214858 residues Searched:

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA Main:*

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11 PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query No. Score Match Length DB ID Description 1 79 100.0 15 4 US-10-001-938-26 Sequence 26, Appl

^	7.0	100 0	0.50	_	10 472 107 1141	~	
2	79	100.0	258	5	US-10-473-127-1141	_	1141, Ap
3	79	100.0	258	5	US-10-473-127-1146	Sequence	1146, Ap
4	79	100.0	397	3	US-09-919-039-178	Sequence	178, App
5	79	100.0	397	5	US-10-473-127-1138	Sequence	1138, Ap
6	79	100.0	397	5	US-10-473-127-1139	Sequence	1139, Ap
7	79	100.0	397	5	US-10-473-127-1140	-	1140, Ap
8	79	100.0	397	5	US-10-473-127-1143	•	1143, Ap
9	79	100.0	397	5	US-10-473-127-1144	Sequence	_
10	. 5 79	100.0	397	5	US-10-473-127-1145	Sequence	•
11	79	100.0	397	5	US-10-756-149-4727	-	•
				5		•	4727, Ap
12	79 70	100.0	397	=	US-10-631-467-559	-	559, App
13	79	100.0	397	5	US-10-631-467-1386	•	1386, Ap
14	79	100.0	397	5	US-10-878-556A-155	-	155, App
15	79	100.0	408	5	US-10-450-763-40099	-	40099, A
16	67	84.8	291	5	US-10-450-763-40097	Sequence	40097, A
17	58	73.4	204	4	US-10-767-701-39910	Sequence	39910, A
18	58	73.4	416	4	US-10-437-963-188385	Sequence	188385,
19	55	69.6	420	4	US-10-437-963-128712	Sequence	128712,
20	55	69.6	420	4	US-10-767-701-46164	•	46164, A
21	55	69.6	433	4	US-10-425-114-63266	Sequence	•
22	55	69.6	435	4	US-10-425-114-59462	Sequence	· ·
23	53	67.1	398	4	US-10-425-114-55344	•	55344, A
24	53	67.1	420	4	US-10-424-599-257607	•	•
				-		Sequence	•
25	53	67.1	420	4	US-10-424-599-257608	Sequence	•
26	53	67.1	424	4	US-10-425-114-46242	-	46242, A
27	52	65.8	422	4	US-10-425-115-332061	Sequence	· ·
28	52	65.8	435	4	US-10-425-114-65366	Sequence	65366, A
29	50	63.3	348	5	US-10-871-388-1	Sequence	1, Appli
30	48	60.8	104	4	US-10-425-115-237886	Sequence	237886,
31	48	60.8	455	4	US-10-369-493-12873	Sequence	12873, A
32	47	59.5	58	4	US-10-424-599-163018	Sequence	163018,
33	47	59.5	340	4	US-10-116-275-134	Sequence	134, App
34	47	59.5	340	4	US-10-116-275-135	-	135, App
35	47	59.5	340	5	US-10-871-388-5	-	5, Appli
36	47	59.5	340	5	US-10-792-571-16		16, Appl
37	47	59.5	340	6	US-11-047-063-2	_	2, Appli
38	47	59.5	345	4	US-10-424-599-275932	Sequence	• •
39	47	59.5	349	5	US-10-732-923-18380	•	· · · · · · · · · · · · · · · · · · ·
40				•		•	18380, A
	47	59.5	377	5	US-10-450-763-48884	•	48884, A
41	46	58.2	334	4	US-10-429-223-3	_	3, Appli
42	46	58.2	337	4	US-10-788-792-162	_	162, App
43	45	57.0	77	4	US-10-106-698-5915	-	5915, Ap
44	45	57.0	389	6	US-11-097-143-20832	Sequence	20832, A
45	45	57.0	403	6	US-11-097-143-24405	Sequence	24405, A
46	45	57.0	403	6	US-11-097-143-41904	Sequence	41904, A
47	45	57.0	412	5	US-10-965-898-18	Sequence	18, Appl
48	45	57.0	479	4	US-10-788-792-186	Sequence	186, App
49	43	54.4	91	4	US-10-425-115-212526	Sequence	212526,
50	43	54.4	104	4	US-10-425-115-314381	Sequence	•
51	43	54.4	392	5	US-10-467-657-1784	-	1784, Ap
52	43	54.4	439	4	US-10-369-493-6325	_	6325, Ap
53	43	54.4	666	4	US-10-724-972A-7129	_	7129, Ap
54	42	53.2	90	4	US-10-425-115-189463	•	•
55	42	53.2		_		Sequence	
			129	4	US-10-425-115-307676	Sequence	· · · · · · · · · · · · · · · · · · ·
56	42	53.2	136	4	US-10-767-701-47402	•	47402, A
57	42	53.2	174	4	US-10-425-115-314374	Sequence	•
58	42	53.2	205	6	US-11-096-568A-21365	•	21365, A
59	42	53.2	206	6	US-11-096-568A-15004	•	15004, A
60	42	53.2	210	4	US-10-425-115-209770	Sequence	209770,
61	42	53.2	228	4	US-10-767-701-46318	•	46318, A
62	42	53.2	228	4	US-10-425-115-314380	Sequence	314380,

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-26.rapbn.

Score Home Page Retrieve Application

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SCORE System
Overview

SCORE FAQ Comments / Suggestions

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-001-938-26.rapbn.

<u>start</u>

Run on:

Go Back to previous pag

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OM protein - protein search, using sw model

June 2, 2006, 19:30:30; Search time 3.57616 Seconds

(without alignments)

48.509 Million cell updates/sec

Title: US-10-001-938-26

Perfect score: 79

Sequence: 1 GRLIIEFKVNFPENG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 58871 segs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database: Published Applications AA New:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /EMC Celerra SIDS3/ptodata/2/pubpaa/PCT NEW PUB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10 NEW PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /EMC Celerra SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

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No.	Score	Match	Length	DB	ID	Description
1	79	100.0	15	6	US-10-490-949-35	Sequence 35, Appl
2	53	67.1	338	6	US-10-953-349-13711	Sequence 13711, A
3	53	67.1	382	6	US-10-953-349-13710	Sequence 13710, A
4	53	67.1	420	6	US-10-953-349-13709	Sequence 13709, A
5	43	54.4	257	6	US-10-953-349-1056	Sequence 1056, Ap
6	43	54.4	337	6	US-10-953-349-1055	Sequence 1055, Ap
7	43	54.4	419	6	US-10-953-349-1054	Sequence 1054, Ap
8	41	51.9	87	6	US-10-953-349-38753	Sequence 38753, A
9	41	51.9	93	6	US-10-953-349-38752	Sequence 38752, A
10	41	51.9	95	6	US-10-953-349-38751	Sequence 38751, A
11	40	50.6	256	6	US-10-953-349-16379	Sequence 16379, A
12	40	50.6	316	6	US-10-953-349-36080	Sequence 36080, A
13	40	50.6	317	6	US-10-953-349-36079	Sequence 36079, A
14	40	50.6	336	6	US-10-953-349-16378	Sequence 16378, A
15	40	50.6	397	7	US-11-293-697-3837	Sequence 3837, Ap
16	40	50.6	417	6	US-10-953-349-16377	Sequence 16377, A
17	40	50.6	426	7	US-11-293-697-4751	Sequence 4751, Ap
18	40	50.6	763	7	US-11-122-986-338	Sequence 338, App
19	40	50.6	763	7	US-11-122-986-340	Sequence 340, App
20	39	49.4	278	6	US-10-953-349-2767	Sequence 2767, Ap
21	39	49.4	304	6	US-10-953-349-2766	Sequence 2766, Ap
22	39	49.4	312	6	US-10-953-349-2765	Sequence 2765, Ap
23	38	48.1	158	6	US-10-953-349-39181	Sequence 39181, A
24	38	48.1	175	6	US-10-953-349-39180	Sequence 39180, A
25	38	48.1	187	6	US-10-953-349-39179	Sequence 39179, A
26	38	48.1	643	6	US-10-504-120-19	Sequence 19, Appl
27	38	48.1	1151	7	US-11-246-999-103	Sequence 103, App
28	38	48.1	1366	6	US-10-985-570-3	Sequence 3, Appli
29	36	45.6	189	6	US-10-953-349-9120	Sequence 9120, Ap
30	36	45.6	192	6	US-10-953-349-9119	Sequence 9119, Ap
31	36	45.6	248	6	US-10-953-349-9118	Sequence 9118, Ap
32	36	45.6	523	6	US-10-953-349-36009	Sequence 36009, A
33	36	45.6	565	6	US-10-953-349-36008	Sequence 36008, A
34 35	36 25	45.6	2209	7	US-11-301-554-1903	Sequence 1903, Ap
35 36	35 35	44.3	213 250	6 6	US-10-953-349-19718	Sequence 19718, A
37	35	44.3	392	6	US-10-953-349-19717 US-10-953-349-5472	Sequence 19717, A
38	35	44.3	511	7	US-11-121-154-96	Sequence 5472, Ap Sequence 96, Appl
39	34	43.0	140	6	US-10-953-349-39676	
40	34	43.0	153	7	US-11-244-348A-6	Sequence 39676, A Sequence 6, Appli
41	34	43.0	243	6	US-10-953-349-39675	Sequence 39675, A
42	34	43.0	308	6	US-10-953-349-19157	Sequence 19157, A
43	34	43.0	334	6	US-10-953-349-9073	Sequence 9073, Ap
44	34	43.0	348	6	US-10-953-349-14087	Sequence 14087, Ap
45	34	43.0	369	6	US-10-953-349-14086	Sequence 14086, A
46	34	43.0	385	6	US-10-953-349-9072	Sequence 9072, Ap
47	34	43.0	390	6	US-10-953-349-9071	Sequence 9071, Ap
48	34	43.0	458	6	US-10-196-749-498	Sequence 498, App
49	34	43.0	464	6	US-10-505-928-757	Sequence 757, App
50	34	43.0	466	6	US-10-953-349-22705	Sequence 22705, A
51	34	43.0	483	6	US-10-953-349-22704	Sequence 22704, A
52	34	43.0	516	6	US-10-953-349-23783	Sequence 23783, A
53	34	43.0	534	6	US-10-953-349-22703	Sequence 22703, A
54	34	43.0	551	7	US-11-236-238-29	Sequence 29, Appl
55	34	43.0	592	6	US-10-953-349-23782	Sequence 23782, A
56	34	43.0	596	6	US-10-953-349-23781	Sequence 23781, A
57	34	43.0	644	7	US-11-244-348A-5	Sequence 5, Appli
58	34	43.0	1025	6	US-10-505-928-505	Sequence 505, App
59	33.5	42.4	230	7	US-11-118-112A-220	Sequence 220, App

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-3.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 3.rai.

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:37:25; Search time 15.5789 Seconds

(without alignments)

89.896 Million cell updates/sec

Title: US-10-001-938-3

Perfect score: 86

Sequence: 1 QKRAAYDQYGHAAFEQ 16

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

650591 seqs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

/EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:* 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/iaa/H_COMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/iaa/PCTUS COMB.pep:* 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

/EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1 2		100.0 100.0	131 131		US-09-553-498-4 US-09-618-869-4	Sequence 4, Appli Sequence 4, Appli

2	0.6	100 0	200	^	va 00 542 6017 5010	C 5010 D.
3	86	100.0	380	2	US-09-543-681A-5912	Sequence 5912, Ap
4	86	100.0	380	2	US-09-489-039A-9011	Sequence 9011, Ap
5	86	100.0	399	2	US-09-553-498-2	Sequence 2, Appli
6	86	100.0	399	2	US-09-618-869-2	Sequence 2, Appli
7	81	94.2	15	1	US-08-618-464-4	Sequence 4, Appli
8	81	94.2	15	2	US-09-107-615-4	Sequence 4, Appli
9	81	94.2	15	2	US-09-756-983-10	Sequence 10, Appl
10	81	94.2	15	2	US-10-299-184A-4	Sequence 4, Appli
11	81	94.2	15	2	US-09-828-574A-10	Sequence 10, Appl
12	81	94.2	15	3	US-09-421-506-10	Sequence 10, Appl
13	81	94.2	15	5	PCT-US95-04896-4	Sequence 4, Appli
14	72	83.7	15	1	US-08-618-464-5	Sequence 5, Appli
15	72	83.7	15	2	US-09-107-615-5	Sequence 5, Appli
16	72	83.7	15	2	US-10-299-184A-5	Sequence 5, Appli
17				2		
	72	83.7	15	_	US-09-828-574A-11	Sequence 11, Appl
18	72	83.7	15	5	PCT-US95-04896-5	Sequence 5, Appli
19	67	77.9	376	3	US-10-375-010-22	Sequence 22, Appl
20	62	72.1	381	2	US-09-252-991A-27174	Sequence 27174, A
21	61	70.9	407	2	US-09-540-236-2899	Sequence 2899, Ap
22	60	69.8	368	2	US-09-861-451A-2	Sequence 2, Appli
23	56	65.1	352	1	US-08-472-534-6	Sequence 6, Appli
24	56	65.1	378	2	US-09-583-110-4647	Sequence 4647, Ap
25	56	65.1	379	2	US-09-107-433-3487	Sequence 3487, Ap
26	54	62.8	15	1	US-08-618-464-6	Sequence 6, Appli
27	54	62.8	15	2	US-09-107-615-6	Sequence 6, Appli
28	54	62.8	15	2	US-10-299-184A-6	Sequence 6, Appli
29	53	61.6	240	2	US-09-248-796A-17703	Sequence 17703, A
30	52	60.5	375	2	US-09-328-352-4984	Sequence 4984, Ap
31	47	54.7	138	2		- · · · · · · · · · · · · · · · · · · ·
				_	US-09-902-540-13689	Sequence 13689, A
32	47	54.7	373	2	US-09-710-279-890	Sequence 890, App
33	47	54.7	385	2	US-09-134-001C-3688	Sequence 3688, Ap
34	47	54.7	595	2	US-10-104-047-2714	Sequence 2714, Ap
35	46	53.5	419	1	US-08-686-417-3	Sequence 3, Appli
36	45	52.3	677	2	US-09-252-991A-18102	Sequence 18102, A
37	44	51.2	387	2	US-09-908-992B-11	Sequence 11, Appl
38	44	51.2	397	2	US-09-248-796A-17628	Sequence 17628, A
39	44	51.2	414	2	US-09-908-992B-10	Sequence 10, Appl
40	44	51.2	452	2	US-09-908-992B-29	Sequence 29, Appl
41	44	51.2	453	2	US-09-908-992B-9	Sequence 9, Appli
42	44	51.2	453	2	US-09-908-992B-30	Sequence 30, Appl
43	44	51.2	479	2	US-09-908-992B-28	Sequence 28, Appl
44	44	51.2	480	2	US-09-908-992B-8	Sequence 8, Appli
45	44	51.2	480	2	US-09-908-992B-12	Sequence 12, Appl
46	44	51.2	915	2	US-09-252-991A-24992	Sequence 24992, A
47	43	50.0	1895	1	US-08-619-554-4	Sequence 4, Appli
48	43	50.0	1895	2	US-09-487-558B-136	Sequence 136, App
49	41	47.7	87	2	US-09-882-835-4	
				_		Sequence 4, Appli
50	41	47.7	191	2	US-10-094-749-2011	Sequence 2011, Ap
51	41	47.7	223	2	US-09-658-644-4	Sequence 4, Appli
52	41	47.7	223	2	US-09-949-016-6832	Sequence 6832, Ap
53	41	47.7	267	2	US-09-949-016-11497	Sequence 11497, A
54	41	47.7	348	1	US-08-974-546-1	Sequence 1, Appli
55	41	47.7	387	2	US-09-543-681A-7130	Sequence 7130, Ap
56	41	47.7	845	2	US-09-252-991A-29230	Sequence 29230, A
57	40	46.5	231	2	US-09-902-540-14837	Sequence 14837, A
58	40	46.5	317	2	US-09-328-352-8169	Sequence 8169, Ap
59	40	46.5	487	2	US-09-252-991A-21980	Sequence 21980, A
60	39	45.3	53	3	US-10-016-768A-2	Sequence 2, Appli
61	39	45.3	116	2	US-09-248-796A-21361	Sequence 21361, A
62	39	45.3	213	2	US-10-094-749-1949	Sequence 1949, Ap
63	39	45.3	442	3	US-10-016-768A-8	Sequence 8, Appli
			- 	_		

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-3.ra

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 3.rapbm.

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:58:51; Search time 67.5789 Seconds

(without alignments)

109.671 Million cell updates/sec

Title: US-10-001-938-3

Perfect score: 86

Sequence: 1 QKRAAYDQYGHAAFEQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database: Published Applications AA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /FMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB_pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
1	86	100.0	16	4	US-10-001-938-3	Sequence 3, Appli
2	86	100.0	340	3	US-09-764-868-1153	Sequence 1153, Ap
3	86	100.0	341	3	US-09-764-868-1152	Sequence 1152, Ap

				_			
4	86	100.0	376	4	US-10-369-493-689	Sequence	689, App
5	86	100.0	376	6	US-11-080-458-32	Sequence	32, Appl
6	86	100.0	378	4	US-10-369-493-386	Sequence	386, App
7	86	100.0	378	4	US-10-369-493-21305	-	21305, A
8	86	100.0	476	5	US-10-450-763-48130	-	48130, A
9	81	94.2	15	3	US-09-756-983-10	•	•
•				_		•	10, Appl
10	81	94.2	15	3	US-09-828-574-10		10, Appl
11	81	94.2	15	4	US-10-001-938-27	Sequence	27, Appl
12	81	94.2	15	4	US-10-299-540-4	Sequence	4, Appli
13	81	94.2	15	4	US-10-299-184-4	Sequence	4, Appli
14	81	94.2	15	4	US-10-239-313A-444	_	444, App
15	81	94.2	15	5	US-10-614-639A-10	-	10, Appl
16	81	94.2	15	5	US-10-614-414A-10	-	
				_		_	10, Appl
17	81	94.2	15	5	US-10-960-855-10	-	10, Appl
18	81	94.2	15	6	US-11-080-458-10	Sequence	10, Appl
19	81	94.2	16	4	US-10-239-313A-447	Sequence	447, App
20	79	91.9	365	4	US-10-369-493-10648	Sequence	10648, A
21	78	90.7	376	4	US-10-369-493-12087		12087, A
22	73	84.9	344	5	US-10-467-657-8284		8284, Ap
23	72	83.7	15	3	US-09-828-574-11	-	
				_		_	11, Appl
24	72	83.7	15	4	US-10-299-540-5	_	5, Appli
25	72	83.7	15	4	US-10-299-184-5	Sequence	5, Appli
26	72	83.7	15	6	US-11-080-458-11	Sequence	11, Appl
27	69	80.2	382	4	US-10-369-493-8065	Sequence	8065, Ap
28	69	80.2	384	4	US-10-369-493-21849	-	21849, A
29	67	77.9	376	4	US-10-375-010-22	•	22, Appl
30	67	77.9	376	6	US-11-232-406A-22	-	
						-	22, Appl
31	67	77.9	379	4	US-10-369-493-7330	-	7330, Ap
32	67	77.9	380	4	US-10-369-493-4573	-	4573, Ap
33	63	73.3	376	4	US-10-369-493-47	Sequence	47, Appl
34	62	72.1	374	4	US-10-369-493-13658	Sequence	13658, A
35	61	70.9	378	4	US-10-369-493-8450	Sequence	8450, Ap
36	61	70.9	385	5	US-10-501-282-4398	-	4398, Ap
37	60	69.8	368	3	US-09-861-451A-2	-	2, Appli
38	60	69.8	375	4	US-10-369-493-15859	-	15859, A
39				_		•	i de la companya de
	60	69.8	376	4	US-10-369-493-15487	-	15487, A
40	59	68.6	358	4	US-10-369-493-9641	-	9641, Ap
41	58	67.4	379	4	US-10-369-493-18523	Sequence	18523, A
42	58	67.4	385	4	US-10-369-493-16754	Sequence	16754, A
43	57	66.3	369	4	US-10-369-493-19646	Sequence	19646, A
44	57	66.3	377	6	US-11-045-004-1504	Seguence	1504, Ap
45	56	65.1	362	4	US-10-369-493-9305	•	9305, Ap
46	56	65.1	378	4	US-10-474-776-634	•	634, App
47	56	65.1	378	5	US-10-472-928-900	_	
				_		_	900, App
48	56	65.1	379	5	US-10-617-320-3487	_	3487, Ap
49	54	62.8	15	4	US-10-299-540-6	Sequence	6, Appli
50	54	62.8	15	4	US-10-299-184-6	Sequence	6, Appli
51	54	62.8	318	4	US-10-425-115-239397	Sequence	239397,
52	53	61.6	423	4	US-10-369-493-12619	Sequence	12619, A
53	52	60.5	360	4	US-10-369-493-10371	•	10371, A
54	52	60.5	372	4	US-10-369-493-23206	•	23206, A
55				_		•	· ·
	52	60.5	376	4	US-10-369-493-1212	•	1212, Ap
56	52	60.5	395	6	US-11-079-463-9803	•	9803, Ap
57	50	58.1	175	4	US-10-767-701-40315	•	40315, A
58	50	58.1	241	4	US-10-425-115-289174	Sequence	289174,
59	50	58.1	297	4	US-10-282-122A-54551	Sequence	54551, A
60	50	58.1	334	6	US-11-096-568A-24300	•	24300, A
61	50	58.1	362	4	US-10-437-963-190831	Sequence	
62	50	58.1	362	4	US-10-425-115-289176	Sequence	
63							
	50 50	58.1	362	6	US-11-096-568A-24299	•	24299, A
64	50	58.1	383	4	US-10-437-963-108162	Sequence	108162,

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-3.rapbn.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

June 2, 2006, 19:45:07; Search time 3.78947 Seconds Run on:

(without alignments)

48.831 Million cell updates/sec

US-10-001-938-3 Title:

Perfect score: 86

1 QKRAAYDQYGHAAFEQ 16 Sequence:

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

58871 seqs, 11565156 residues Searched:

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Published Applications AA New:* Database:

/EMC Celerra SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:* 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10 NEW PUB.pep:*

7: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

&

No.	Score	Match	Length	DB	ID	Description
1	86	100.0	16	6	US-10-490-949-4	Sequence 4, Appli
2	81	94.2	15	6	US-10-490-949-10	Sequence 10, Appl
3	72	83.7	15	6	US-10-490-949-11	Sequence 11, Appl
4	63	73.3	389	7	US-11-122-986-185	Sequence 185, App
5	63	73.3	389	7	US-11-122-986-187	Sequence 187, App
6	59	68.6	332	6	US-10-953-349-1407	Sequence 1407, Ap
7	59	68.6	367	6	US-10-953-349-1406	Sequence 1406, Ap
8	59	68.6	456	6	US-10-953-349-1405	Sequence 1405, Ap
9	54	62.8	15	6	US-10-490-949-1	Sequence 1, Appli
10	49	57.0	307	6	US-10-953-349-2183	Sequence 2183, Ap
11	49	57.0	335	6	US-10-953-349-2182	Sequence 2182, Ap
12	49	57.0	343	6	US-10-953-349-2181	Sequence 2181, Ap
13	48	55.8	141	6	US-10-953-349-10348	Sequence 10348, A
14	46	53.5	186	6	US-10-953-349-16110	Sequence 16110, A
15	46	53.5	419	6	US-10-953-349-1054	Sequence 1054, Ap
16	43	50.0	308	6	US-10-953-349-33811	Sequence 33811, A
17	43	50.0	336	6	US-10-953-349-33810	Sequence 33810, A
18	43	50.0	430	6	US-10-953-349-33809	Sequence 33809, A
19	42	48.8	339	6	US-10-953-349-12422	Sequence 12422, A
20	42	48.8	382	6	US-10-953-349-13710	Sequence 13710, A
21	42	48.8	420	6	US-10-953-349-13709	Sequence 13709, A
22	41	47.7	321	6	US-10-953-349-950	Sequence 950, App
23	41	47.7	323	6	US-10-953-349-949	Sequence 949, App
24	41	47.7	346	6	US-10-953-349-4235	Sequence 4235, Ap
25	41	47.7	349	6	US-10-953-349-948	Sequence 948, App
26 27	41 41	47.7 47.7	363 380	6 6	US-10-953-349-4234 US-10-953-349-7175	Sequence 4234, Ap
28	41	47.7	381	6	US-10-953-349-7173	Sequence 7175, Ap Sequence 4233, Ap
29	41	47.7	391	6	US-10-953-349-7174	Sequence 7174, Ap
30	41	47.7	442	6	US-10-953-349-7174	Sequence 7174, Ap
31	40	46.5	417	6	US-10-953-349-16377	Sequence 16377, Ap
32	39	45.3	1386	7	US-11-314-018-6	Sequence 6, Appli
33	38	44.2	166	6	US-10-953-349-16554	Sequence 16554, A
34	38	44.2	221	6	US-10-953-349-16553	Sequence 16553, A
35	38	44.2	231	6	US-10-953-349-16552	Sequence 16552, A
36	36	41.9	74	6	US-10-953-349-14225	Sequence 14225, A
37	36	41.9	96	6	US-10-953-349-14224	Sequence 14224, A
38	36	41.9	270	6	US-10-953-349-29919	Sequence 29919, A
39	36	41.9	295	6	US-10-953-349-29918	Sequence 29918, A
40	36	41.9	341	6	US-10-953-349-29917	Sequence 29917, A
41	36	41.9	397	7	US-11-293-697-3837	Sequence 3837, Ap
42	36	41.9	426	7	US-11-293-697-4751	Sequence 4751, Ap
43	35	40.7	179	6	US-10-953-349-7415	Sequence 7415, Ap
44	35	40.7	189	6	US-10-953-349-9120	Sequence 9120, Ap
45	35	40.7	189	7	US-11-293-697-4556	Sequence 4556, Ap
46	35	40.7	192	6	US-10-953-349-9119	Sequence 9119, Ap
47	35	40.7	230	6	US-10-953-349-7414	Sequence 7414, Ap
48	35	40.7	248	6	US-10-953-349-9118	Sequence 9118, Ap
49	35	40.7	271	6	US-10-953-349-18081	Sequence 18081, A
50	35	40.7	273	6	US-10-953-349-18080	Sequence 18080, A
51	35	40.7	314	6	US-10-953-349-18079	Sequence 18079, A
52	35	40.7	357	6	US-10-953-349-2047	Sequence 2047, Ap
53	35	40.7	361	6	US-10-953-349-2046	Sequence 2046, Ap
54	35	40.7	731	7	US-11-293-697-3006	Sequence 3006, Ap
55 56	34	39.5	15		US-10-490-949-16	Sequence 16, Appl
56 57	34	39.5	15	6	US-10-490-949-17	Sequence 17, Appl
57 58	34	39.5	89 174	6	US-10-953-349-36746	Sequence 36746, A
58 59	34 34	39.5 39.5	174 211	6 6	US-10-953-349-15236 US-10-953-349-27572	Sequence 15236, A Sequence 27572, A
JJ	24	J9.J	211	O	00 10-300-343-61316	sequence 21312, A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-4.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 4.rai.

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OM protein - protein search, using sw model

June 2, 2006, 19:08:52; Search time 11.4238 Seconds Run on:

(without alignments)

114.932 Million cell updates/sec

Title: US-10-001-938-4

Perfect score: 90

Sequence: 1 QGFFAVQQTCPHCQG 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

650591 seqs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6_COMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:* 4: /EMC Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/iaa/PCTUS COMB.pep:* 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

/EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description		
1 2	90 90	100.0	380		US-09-489-039A-9011 US-09-553-498-2	Sequence 9011, Ap Sequence 2, Appli		

•		4000	0.00	_		_	
3	90	100.0	399	2	US-09-618-869-2	_	2, Appli
4	74	82.2	381	2	US-09-252-991A-27174	_	27174, A
5	73	81.1	376	3	US-10-375-010-22	•	22, Appl
6	69	76.7	407	2	US-09-540-236-2899	Sequence	2899, Ap
7	65	72.2	380	2	US-09-543-681A-5912	Sequence	5912, Ap
8	64	71.1	375	2	US-09-328-352-4984	Sequence	4984, Ap
9	54	60.0	392	2	US-09-198-452A-48	Sequence	48, Appl
10	54	60.0	406	2	US-09-438-185A-34	Sequence	34, Appl
11	50	55.6	209	2	US-09-902-540-14118	-	14118, A
12	45	50.0	858	2	US-09-960-428-7	•	7, Appli
13	44	48.9	108	2	US-09-328-352-5857		5857, Ap
14	44	48.9	125	2	US-09-328-352-7243	•	7243, Ap
15	44	48.9	132	2	US-09-513-999C-6410		· -
16				2		Sequence	•
	44	48.9	354		US-09-583-110-4854	Sequence	
17	44	48.9	364	2	US-09-107-433-4701	•	4701, Ap
18	44	48.9	635	2	US-10-104-047-2128		2128, Ap
19	44	48.9	1007	2	US-09-252-991A-28773	•	28773, A
20	43	47.8	110	2	US-08-858-207A-273	Sequence	273, App
21	43	47.8	115	2	US-09-583-110-3398	Sequence	3398, Ap
22	43	47.8	120	2	US-09-107-433-3440	Sequence	3440, Ap
23	43	47.8	296	2	US-09-270-767-57017	Sequence	57017, A
24	43	47.8	369	2	US-09-270-767-41773	Sequence	41773, A
25	43	47.8	505	2	US-09-489-039A-12262	Sequence	12262, A
26	42	46.7	350	2	US-09-252-991A-27255	_	27255, A
27	42	46.7	952	2	US-10-216-556A-2	•	2, Appli
28	41	45.6	119	2	US-09-598-747-2	_	2, Appli
29	41	45.6	186	2	US-09-248-796A-15844	_	15844, A
30	41	45.6	1404	2	US-09-345-473E-24	-	24, Appl
31	41	45.6		_		-	•
			1404	2	US-09-862-027-24	-	24, Appl
32	40	44.4	66	2	US-09-248-796A-27118	-	27118, A
33	40	44.4	81	2	US-09-543-681A-6756	-	6756, Ap
34	40	44.4	118	2	US-09-621-976-4089	-	4089, Ap
35	40	44.4	288	. 2	US-09-949-016-7274	—	7274, Ap
36	40	44.4	288	2	US-09-964-899-21	-	21, Appl
37	40	44.4	373	2	US-09-710-279-890	Sequence	890, App
38	40	44.4	385	2	US-09-134-001C-3688	Sequence	3688, Ap
39	40	44.4	459	2	US-09-252-991A-32058	Sequence	32058, A
40	40	44.4	644	2	US-09-605-042A-38	Sequence	38, Appl
41	40	44.4	2789	2	US-09-949-016-8208	Sequence	8208, Ap
42	40	44.4	2871	2	US-09-538-092-1076	Sequence	1076, Ap
43	39	43.3	60	2	US-09-270-767-58063	Sequence	58063, A
44	39	43.3	164	2	US-10-094-749-2758	•	2758, Ap
45	39	43.3	262	2	US-10-094-749-2390	Sequence	•
46	39	43.3	283	2	US-10-104-047-2687	Sequence	· · · · · · · · · · · · · · · · · · ·
47	39	43.3	290	2	US-10-094-749-2565	-	2565, Ap
48	39	43.3	303	2	US-09-248-796A-15837	•	15837, A
49	39	43.3	462	2	US-09-489-039A-12291	-	12291, A
50	39	43.3	508	2	US-09-134-001C-4570	-	4570, Ap
51	39	43.3	510	1	US-08-220-677A-2	-	2, Appli
				_		-	
52	39.		512	2	US-09-107-532A-6559	-	6559, Ap
53	39	43.3	522	2	US-09-252-991A-28463	-	28463, A
54	39	43.3	523	2	US-09-328-352-6394	•	6394, Ap
55	39	43.3	523	2	US-09-328-352-6395	•	6395, Ap
56	39	43.3	524	2	US-09-540-236-2706	-	2706, Ap
57	39	43.3	538	2	US-09-543-681A-4490	-	4490, Ap
58	39	43.3	545	2	US-09-019-095A-38	Sequence	38, Appl
59	39	43.3	606	2	US-09-134-000C-4093	Sequence	4093, Ap
60	39	43.3	614	2	US-09-949-016-8536	Sequence	8536, Ap
61	39	43.3	640	2	US-09-605-042A-40	Sequence	40, Appl
62	39	43.3	673	2	US-10-104-047-2774	Sequence	2774, Ap
63	39	43.3	816	1	US-08-820-170A-37	_	37, Appl
						•	• •

SCORE Search Results Details for Application 10 Search Result us-10-001-938-4.rapbn

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 start

GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2006, 19:29:53; Search time 75.9934 Seconds

(without alignments)

91.432 Million cell updates/sec

Title: US-10-001-938-4

Perfect score: 90

Sequence: 1 QGFFAVQQTCPHCQG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database: Published Applications AA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length D)B	ID	Description
1	90	100.0	15	4	US-10-001-938-4	Sequence 4, Appli
2	90	100.0	340	3	US-09-764-868-1153	Sequence 1153, Ap
3	90	100.0	341	3	US-09-764-868-1152	Sequence 1152, Ap
4	90	100.0	376	4	US-10-369-493-689	Sequence 689, App

c	0.0	100 0	276	6	HG 11 000 4E0 22	0	D 1
5	90	100.0	376	6	US-11-080-458-32	Sequence 32	
6	90	100.0	832	5	US-10-450-763-59430	Sequence 59	·
7	78	86.7	369	4	US-10-369-493-19646	Sequence 19	646, A
8	74	82.2	374	4	US-10-369-493-13658	Sequence 13	658, A
9	73	81.1	376	4	US-10-375-010-22	Sequence 22	, Appl
10	73	81.1	376	6	US-11-232-406A-22	Sequence 22	, Appl
11	72	80.0	379	4	US-10-369-493-7330	Sequence 73	
12	72	80.0	380	4	US-10-369-493-4573	Sequence 45	• -
13	71	78.9	376	4	US-10-369-493-12087	Sequence 12	•
14	70	77.8	362	4	US-10-369-493-9305	Sequence 93	•
15	69	76.7	378	4	US-10-369-493-8450	•	•
				_		Sequence 84	•
16	68	75.6	375	4	US-10-369-493-15859	Sequence 15	·
17	68	75.6	376	4	US-10-369-493-15487	Sequence 15	•
18	67	74.4	378	4	US-10-369-493-386	Sequence 38	
19	67	74.4	378	4	US-10-369-493-21305	Sequence 21	305, A
20	64	71.1	382	4	US-10-369-493-8065	Sequence 80	65, Ap
21	61	67.8	385	4	US-10-369-493-16754	Sequence 16	754, A
22	60	66.7	365	4	US-10-369-493-10648	Sequence 10	648, A
23	57	63.3	384	4	US-10-369-493-21849	Sequence 21	= /
24	56	62.2	344	5	US-10-467-657-8284	Sequence 82	•
25	54	60.0	392	4	US-10-289-762-48	Sequence 48	•
26	53	58.9	339	4	US-10-369-493-19527	Sequence 19	
				_		•	·
27	53	58.9	376	4	US-10-369-493-47	Sequence 47	
28	51	56.7	274	4	US-10-335-977-7665	Sequence 76	•
29	51	56.7	275	4	US-10-335-977-7664	Sequence 76	_
30	51	56.7	369	3	US-09-895-913A-180	Sequence 18	
31	51	56.7	369	4	US-10-335-977-7666	Sequence 76	66, Ap
32	50	55.6	666	6	US-11-098-686-11016	Sequence 11	016, A
33	49	54.4	123	3	US-09-867-550-1492	Sequence 14	92, Ap
34	49	54.4	275	4	US-10-158-057-230	Sequence 23	0, App
35	49	54.4	385	5	US-10-501-282-4398	Sequence 43	98, Ap
36	47	52.2	97	4	US-10-437-963-199043	Sequence 19	-
37	47	52.2	140	4	US-10-424-599-151787	Sequence 15	•
38	47	52.2	198	5	US-10-204-921-70	Sequence 70	•
39	47	52.2	572	4	US-10-267-502-268	Sequence 26	
40	46	51.1	107	4	US-10-453-468-4	-	
				_		Sequence 4,	
41	46	51.1	261	5	US-10-631-467-702	Sequence 70	
42	46	51.1	374	6	US-11-087-099-5695	Sequence 56	•
43	45	50.0	225	4	US-10-424-599-166583	Sequence 16	•
44	45	50.0	608	4	US-10-161-493-112	Sequence 11	
45	45	50.0	769	4	US-10-437-963-129386	Sequence 12	•
46	45	50.0	858	3	US-09-960-428-7	Sequence 7,	Appli
47	45	50.0	1437	5	US-10-684-141-44	Sequence 44	, Appl
48	45	50.0	1437	5	US-10-810-486-44	Sequence 44	, Appl
49	44	48.9	97	4	US-10-425-115-259098	Sequence 25	9098,
50	44	48.9	101	4	US-10-282-122A-44927	Sequence 44	927, A
51	44	48.9	112	5	US-10-450-763-58103	Sequence 58	Ē
52	44	48.9	226	3	US-09-971-361-11	Sequence 11	
53	44	48.9	226	6	US-11-108-870-11	Sequence 11	
54	44	48.9	298	6	US-11-097-143-21180	Sequence 21	
						-	· ·
55	44	48.9	354	5	US-10-472-928-60	Sequence 60	• • •
56	44	48.9	364	5	US-10-617-320-4701	Sequence 47	-
57	44	48.9	511	4	US-10-369-493-21871	Sequence 21	
58	44	48.9	513	6	US-11-097-143-11568	Sequence 11	
59	44	48.9	635	4	US-10-104-047-2128	Sequence 21	•
60	44	48.9	635	6	US-11-072-512-2128	Sequence 21	•
61	44	48.9	660	4	US-10-282-122A-47186	Sequence 47	186, A
62	43	47.8	79	4	US-10-425-115-193883	Sequence 19	3883,
63	43	47.8	89	4	US-10-425-115-351689	Sequence 35	1689,
64	43	47.8	115	4	US-10-425-115-200172	Sequence 20	
65	43	47.8	115	5	US-10-472-928-3058	Sequence 30	· · · · · · · · · · · · · · · · · · ·
	- -		=	-		4	

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-4.rapbn.

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SCORE FAQ

Comments / **Suggestions**

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 938-4.rapbn.

start

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:30:30; Search time 3.57616 Seconds

(without alignments)

48.509 Million cell updates/sec

Title:

US-10-001-938-4

Perfect score: 90

Sequence:

1 QGFFAVQQTCPHCQG 15

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New:*

/EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /EMC Celerra SIDS3/ptodata/2/pubpaa/PCT NEW PUB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10 NEW PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11 NEW PUB.pep:*

8: /EMC Celerra SIDS3/ptodata/2/pubpaa/US60 NEW PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

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No.	Score	Match	Length	DB	ID	Description
1	90	100.0	15	6	US-10-490-949-5	Sequence 5, Appli
2	42	46.7	361	6	US-10-953-349-17037	Sequence 17037, A
3	42	46.7	375	6	US-10-953-349-17036	Sequence 17036, A
4	41	45.6	232	6	US-10-953-349-17867	Sequence 17867, A
5	41	45.6	244	6	US-10-953-349-17866	Sequence 17866, A
6	40	44.4	332	6	US-10-953-349-1407	Sequence 1407, Ap
7	40	44.4	360	6	US-10-953-349-38192	Sequence 38192, A
8	40	44.4	367	6	US-10-953-349-1406	Sequence 1406, Ap
9	40	44.4	451	6	US-10-953-349-38191	Sequence 38191, A
10	40	44.4	456	6	US-10-953-349-1405	Sequence 1405, Ap
11	39.5	43.9	225	7	US-11-293-697-4687	Sequence 4687, Ap
12	39	43.3	26	1	US-09-949-925-296	Sequence 296, App
13	39	43.3	79	1	US-09-949-925-294	Sequence 294, App
14	39	43.3	255	1	US-09-949-925-297	Sequence 297, App
15	39	43.3	457	6	US-10-953-349-13696	Sequence 13696, A
16	39	43.3	552	6	US-10-953-349-13695	Sequence 13695, A
17	39	43.3	577	7	US-11-293-697-3485	Sequence 3485, Ap
18	39	43.3	578	6	US-10-953-349-13694	Sequence 13694, A
19	39	43.3	724	7	US-11-293-697-3263	Sequence 3263, Ap
20	39	43.3	836	6	US-10-509-131-35	Sequence 35, Appl
21	39	43.3	836	7	US-11-293-697-3700	Sequence 3700, Ap
22	38	42.2	236	6	US-10-933-854-24	Sequence 24, Appl
23	38	42.2	691	6	US-10-511-937-2995	Sequence 2995, Ap
24	38	42.2	706	7	US-11-293-697-3919	Sequence 3919, Ap
25	37	41.1	256	6	US-10-623-808-6	Sequence 6, Appli
26	37	41.1	286	6	US-10-953-349-16858	Sequence 16858, A
27	37	41.1	302	6	US-10-953-349-16857	Sequence 16857, A
28 29	37 37	41.1	308 338	6 6	US-10-953-349-16856 US-10-953-349-13711	Sequence 16856, A Sequence 13711, A
30	37	41.1	339	6	US-10-953-349-19392	Sequence 19392, A
31	3 <i>1</i> 37	41.1	382	6	US-10-953-349-13710	Sequence 13710, A
32	37	41.1	420	6	US-10-953-349-13710	Sequence 13710, A
33	37	41.1	442	6	US-10-953-349-19391	Sequence 19391, A
34	36.5	40.6	97	6	US-10-953-349-16420	Sequence 16420, A
35	36.5	40.6	190	7	US-11-293-697-3234	Sequence 3234, Ap
36	36	40.0	84	7	US-11-328-747-5	Sequence 5, Appli
37	36	40.0	97	6	US-10-953-349-34432	Sequence 34432, A
38	36	40.0	211	6.		Sequence 38932, A
39	36	40.0	214	6	US-10-953-349-9238	Sequence 9238, Ap
40	36	40.0	215	6	US-10-953-349-9237	Sequence 9237, Ap
41	36	40.0	306	7	US-11-249-111-110	Sequence 110, App
42	36	40.0	318	6	US-10-953-349-12208	Sequence 12208, A
43	36	40.0	320	6	US-10-953-349-20561	Sequence 20561, A
44	36	40.0	324	6	US-10-953-349-12207	Sequence 12207, A
45	36	40.0	326	6	US-10-953-349-20560	Sequence 20560, A
46	36	40.0	362	7	US-11-293-697-2645	Sequence 2645, Ap
47	36	40.0	481	7	US-11-293-697-4458	Sequence 4458, Ap
48	36	40.0	549	7	US-11-293-697-4179	Sequence 4179, Ap
49	36	40.0	1912	6	US-10-511-937-2561	Sequence 2561, Ap
50	35.5	39.4	452	7	US-11-326-489-5	Sequence 5, Appli
51	35	38.9		7	US-11-311-555-6	Sequence 6, Appli
52	35	38.9		7	US-11-311-561-6	Sequence 6, Appli
53	35	38.9	177	7	US-11-101-316-156	Sequence 156, App
54	35	38.9			US-10-953-349-38933	Sequence 38933, A
55	35	38.9	253		US-10-953-349-19102	Sequence 19102, A
56	35	38.9			US-11-101-316-8	Sequence 8, Appli
57	35	38.9			US-10-505-928-163	Sequence 163, App
58 5.0	35	38.9			US-10-953-349-427	Sequence 427, App
59	35	38.9	757	6	US-10-953-349-426	Sequence 426, App

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-5.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 5.rai.

<u>start</u>

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

June 2, 2006, 19:12:07; Search time 12.7 Seconds Run on:

(without alignments)

103.383 Million cell updates/sec

Title: US-10-001-938-5

Perfect score: 73

1 SKTLSVKIPGAVDTG 15 Sequence:

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

650591 seqs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:* 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:* /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description	
1 2	63 63	86.3 86.3	399 399	_	US-09-553-498-2 US-09-618-869-2	Sequence 2, Appli Sequence 2, Appli	

						_	
3	60	82.2	380	2	US-09-489-039A-9011	•	9011, Ap
4	59	80.8	380	2	US-09-543-681A-5912	•	5912, Ap
5	58	79.5	381	2	US-09-252-991A-27174	Sequence	27174, A
6	51	69.9	376	3	US-10-375-010-22	Sequence	22, Appl
7	43	58.9	254	2	US-09-248-796A-17877	Sequence	17877, A
8	41	56.2	170	2	US-09-270-767-43106	Sequence	43106, A
9	41	56.2	308	2	US-09-489-039A-8590	Sequence	8590, Ap
10	41	56.2	320	2	US-09-543-681A-7884	Sequence	7884, Ap
11	40	54.8	375	2	US-09-328-352-4984	•	4984, Ap
12	40	54.8	407	2	US-09-540-236-2899	-	2899, Ap
13	39	53.4	62	2	US-09-489-039A-11677	-	11677, A
14	39	53.4	209	2	US-09-902-540-14118	•	14118, A
15	39	53.4	391	2	US-09-902-540-11110	-	į
						-	11110, A
16	39	53.4	595	2	US-09-248-796A-16455	•	16455, A
17	38	52.1	206	2	US-09-270-767-32859	-	32859, A
18	38	52.1	217	2	US-09-489-039A-7245	-	7245, Ap
19	38	52.1	309	2	US-09-489-039A-10229	•	10229, A
20	38	52.1	352	1	US-08-472-534-6	Sequence	6, Appli
21	38	52.1	364	1	US-08-570-311-26	Sequence	26, Appl
22	38	52.1	378	2	US-09-583-110-4647	Sequence	4647, Ap
23	38	52.1	379	2	US-09-107-433-3487	Sequence	3487, Ap
24	38	52.1	905	2	US-09-248-796A-15706	Sequence	15706, A
25	38	52.1	942	1	US-08-141-324-14	-	14, Appl
26	38	52.1	942	1	US-08-541-902-14	Sequence	
27	38	52.1	1732	1	US-08-570-311-10	•	10, Appl
28	38	52.1	1732	1	US-08-353-485-10	_	10, Appl
29	38	52.1	1732	2	US-09-066-330-11		11, Appl
30	37	50.7	233	1	US-08-221-750A-7	•	7, Appli
				_		•	• • •
31	37	50.7	266	2	US-09-252-991A-29750	•	29750, A
32	37	50.7	320	2	US-09-328-352-7937	•	7937, Ap
33	37	50.7	340	2	US-09-107-532A-7298	•	7298, Ap
34	37	50.7	395	2	US-09-712-363-164	•	164, App
35	37	50.7	493	2	US-09-613-303-19	•	19, Appl
36	37	50.7	493	2	US-10-267-311-19	Sequence	19, Appl
37	37	50.7	606	2	US-09-248-796A-17830	Sequence	17830, A
38	37	50.7	903	2	US-09-270-767-46470	Sequence	46470, A
39	36.5	50.0	397	2	US-09-902-540-12830	Sequence	12830, A
40	36	49.3	128	2	US-08-858-207A-314	Sequence	314, App
41	36	49.3	154	2	US-09-248-796A-20059	Sequence	20059, A
42	36	49.3	223	2	US-10-036-041-61	Sequence	61, Appl
43	36	49.3	227	2	US-09-208-718-3	_	3, Appli
44	36	49.3	227	2	US-09-621-976-8	_	8, Appli
45	36	49.3	227	2	US-09-513-999C-8	Sequence	
46	36	49.3	227	2	US-09-471-276-8	_	8, Appli
47	36	49.3	273	2	US-09-198-452A-767		767, App
48	36	49.3	273	2	US-09-438-185A-723		723, App
49	36	49.3	360	2	US-09-543-681A-4783	-	4783, Ap
50	36	49.3	395	2	US-09-603-208A-28	•	•
						_	28, Appl
51	36	49.3	485	2	US-09-902-540-9878	•	9878, Ap
52	36	49.3	664	2	US-09-489-039A-14017	_	14017, A
53	35	47.9	18	1	US-08-468-674B-8	•	8, Appli
54	35	47.9	18	1	US-08-780-571-8		8, Appli
55	35	47.9	18	2	US-09-324-217B-10	-	10, Appl
56	35	47.9	108	2	US-09-187-859-43		43, Appl
57	35	47.9	108	2	US-09-839-542B-43	Sequence	43, Appl
58	35	47.9	108	2	US-09-535-852-43	Sequence	43, Appl
59	35	47.9	108	2	US-10-006-869-43	Sequence	43, Appl
60	35	47.9	188	2	US-09-902-540-14832	Sequence	14832, A
61	35	47.9	271	2	US-09-248-796A-16496	•	16496, A
62	35	47.9	310	2	US-09-614-912-202	•	202, App
63	35	47.9	344	2	US-09-489-039A-14341	•	14341, A
		-		_		, 	

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-5.ra

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 5.rapbm.

<u>start</u>

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:45:16; Search time 63.4 Seconds

(without alignments)

109.593 Million cell updates/sec

Title: US-10-001-938-5

Perfect score: 73

Sequence: 1 SKTLSVKIPGAVDTG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 segs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database: Published Applications AA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
1	73	100.0	15	4	US-10-001-938-5	Sequence 5, Appli
2	63	86.3	340	3	US-09-764-868-1153	Sequence 1153, Ap
3	63	86.3	341	3	US-09-764-868-1152	Sequence 1152, Ap

4	63	86.3	376	4	US-10-369-493-689	Sequence	689, App
5	63	86.3	376	6	US-11-080-458-32	Sequence	32, Appl
6	63	86.3	832	5	US-10-450-763-59430	Sequence	59430, A
7	59	80.8	378	4	US-10-369-493-386	-	386, App
8	59	80.8	378	4	US-10-369-493-21305	-	
						•	21305, A
9	58	79.5	374	4	US-10-369-493-13658	•	13658, A
10	54	74.0	362	4	US-10-369-493-9305	Sequence	9305, Ap
11	52	71.2	375	4	US-10-369-493-15859	Sequence	15859, A
12	52	71.2	376	4	US-10-369-493-15487	-	15487, A
13	51	69.9	376	4	US-10-375-010-22	-	22, Appl
				_		-	
14	51	69.9	376	6	US-11-232-406A-22	-	22, Appl
15	50	68.5	288	4	US-10-369-493-8874	Sequence	8874, Ap
16	50	68.5	369	4	US-10-369-493-19646	Sequence	19646, A
17	49	67.1	379	4	US-10-369-493-7330	Sequence	7330, Ap
18	49	67.1	380	4	US-10-369-493-4573	-	4573, Ap
19	48	65.8	378	4	US-10-156-761-13102	•	13102, A
						•	
20	48	65.8	378	4	US-10-369-493-8450	•	8450, Ap
21	47	64.4	384	4	US-10-369-493-21849	Sequence	21849, A
22	47	64.4	461	4	US-10-424-599-254411	Sequence	254411,
23	45	61.6	306	4	US-10-282-122A-73201	Sequence	73201, A
24	45	61.6	306	4	US-10-282-122A-76109	•	76109, A
				_		_	•
25	45	61.6	343	5	US-10-972-024-277	_	277, App
26	44	60.3	306	4	US-10-369-493-790	Sequence	790, App
27	44	60.3	306	4	US-10-282-122A-42884	Sequence	42884, A
28	44	60.3	374	4	US-10-424-599-253712	Sequence	253712,
29	44	60.3	448	4	US-10-425-115-195339	Sequence	•
30	44	60.3	478	4	US-10-425-114-65215	-	65215, A
31				_		•	•
	43	58.9	305	4	US-10-369-493-13684	_	13684, A
32	43	58.9	376	4	US-10-369-493-1212	-	1212, Ap
33	43	58.9	382	4	US-10-369-493-8065	Sequence	8065, Ap
34	42	57.5	319	4	US-10-282-122A-69287	Sequence	69287, A
35	42	57.5	350	4	US-10-369-493-21024	Sequence	21024, A
36	42	57.5	401	4	US-10-369-493-3465		3465, Ap
37	42	57.5	597	4	US-10-425-114-55831	•	•
				-		-	55831, A
38	42	57.5	665	4	US-10-425-115-323605	Sequence	•
39	42	57.5	852	4	US-10-369-493-1645	Sequence	1645, Ap
40	41	56.2	53	4	US-10-016-157A-229	Sequence	229, App
41	41	56.2	53	6	US-11-042-241-229	Sequence	229, App
42	41	56.2	147	4	US-10-425-115-267989	Sequence	
43	41	56.2	305	4	US-10-282-122A-59632	•	59632, A
44	41	56.2		4		•	•
			314	•	US-10-282-122A-69193	•	69193, A
45	41	56.2	319	4	US-10-282-122A-68006	-	68006, A
46	41	56.2	385	4	US-10-369-493-16754	Sequence	16754, A
47	41	56.2	423	4	US-10-369-493-12619	Sequence	12619, A
48	41	56.2	683	5	US-10-473-127-511	Seguence	511, App
49	41	56.2	683	5	US-10-473-127-512	-	512, App
50	41	56.2	683	5	US-10-473-127-513	-	513, App
						_	
51	41	56.2	683	5	US-10-473-127-514	_	514, App
52	41	56.2	683	5	US-10-473-127-515	•	515, App
53	41	56.2	683	5	US-10-473-127-516	Sequence	516, App
54	41	56.2	683	6	US-11-009-554-9	Sequence	9, Appli
55	41	56.2	905	4	US-10-451-467A-64	-	64, Appl
56	41	56.2	913	6	US-11-097-143-4134	•	4134, Ap
57				5	US-10-745-237-190	-	_
	41	56.2	8943			-	190, App
58	40	54.8	125	4	US-10-156-761-11979	-	11979, A
59	40	54.8	228	4	US-10-437-963-189989	Sequence	•
60	40	54.8	296	4	US-10-282-122A-61258	Sequence	61258, A
61	40	54.8	312	4	US-10-282-122A-50995	Sequence	50995, A
62	40	54.8	344	5	US-10-467-657-8284	-	8284, Ap
63	40	54.8	674	4	US-10-369-493-12648	-	12648, A
64	39.5	54.1	751	3	US-09-795-693-14	•	
0-3	JJ.J	74.I	, 31	3	00 03-133-033-T4	sequence	14, Appl

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-5.rapbn.

Score HomeRetrieve ApplicationSCORE SystemSCOREComments /PageListOverviewFAQSuggestions

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-001-938-5.rapbn.

<u>start</u>

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:44:08; Search time 3.1 Seconds

(without alignments)

55.960 Million cell updates/sec

Title: US-10-001-938-5

Perfect score: 73

Sequence: 1 SKTLSVKIPGAVDTG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database: Published Applications AA New:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /EMC Celerra SIDS3/ptodata/2/pubpaa/PCT NEW PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /EMC Celerra SIDS3/ptodata/2/pubpaa/US60 NEW PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No.	Score	Match	Length	DB	ID	Description
1	73	100.0	15	6	US-10-490-949-6	Sequence 6, Appli
2	44	60.3	202	6	US-10-953-349-11146	Sequence 11146, A
3	44	60.3	219	6	US-10-953-349-11145	Sequence 11145, A
4	44	60.3	222	6	US-10-953-349-11144	Sequence 11144, A
5	44	60.3	380	6	US-10-953-349-7175	Sequence 7175, Ap
6	44	60.3	391	6	US-10-953-349-7174	Sequence 7174, Ap
7	44	60.3	442	6	US-10-953-349-7173	Sequence 7173, Ap
8	38	52.1	354	6	US-10-953-349-4966	Sequence 4966, Ap
9	38	52.1	432	6	US-10-953-349-4965	Sequence 4965, Ap
10	38	52.1	502	6	US-10-953-349-4964	Sequence 4964, Ap
11	35	47.9	371	6	US-10-953-349-10961	Sequence 10961, A
12	35	47.9	457	6	US-10-953-349-10960	Sequence 10960, A
13	35	47.9	490	6	US-10-953-349-10959	Sequence 10959, A
14	35	47.9	5738	6	US-10-505-928-150	Sequence 150, App
15 16	34	46.6	118	7	US-11-293-697-2755	Sequence 2755, Ap
16 17	34	46.6	209	6	US-10-953-349-29859	Sequence 29859, A
17	34	46.6	267	6	US-10-953-349-29858	Sequence 29858, A
18 19	34 34	46.6 46.6	293 545	6 7	US-10-953-349-29857 US-11-293-697-2487	Sequence 29857, A
20	33	45.2	188	6	US-10-953-349-16041	Sequence 2487, Ap Sequence 16041, A
21	33	45.2	273	6	US-10-953-349-16041 US-10-953-349-34506	Sequence 34506, A
22	33	45.2	285	6	US-10-953-349-13230	Sequence 13230, A
23	33	45.2	297	6	US-10-953-349-16040	Sequence 16040, A
24	33	45.2	300	6	US-10-953-349-16039	Sequence 16039, A
25	33	45.2	303	6	US-10-953-349-34505	Sequence 34505, A
26	33	45.2	315	6	US-10-953-349-4747	Sequence 4747, Ap
27	33	45.2	319	6	US-10-953-349-5745	Sequence 5745, Ap
28	33	45.2	335	6	US-10-953-349-13229	Sequence 13229, A
29	33	45.2	341	6	US-10-953-349-5744	Sequence 5744, Ap
30	33	45.2	347	6	US-10-953-349-13228	Sequence 13228, A
31	33	45.2	391	6	US-10-953-349-5743	Sequence 5743, Ap
32	33	45.2	428	6	US-10-196-749-514	Sequence 514, App
33	33	45.2	436	6	US-10-953-349-4746	Sequence 4746, Ap
34	33	45.2	465	6	US-10-953-349-4745	Sequence 4745, Ap
35	33	45.2	534	7	US-11-121-154-135	Sequence 135, App
36	32	43.8	134	6	US-10-953-349-15674	Sequence 15674, A
37	32	43.8	154	6	US-10-953-349-13884	Sequence 13884, A
38	32	43.8	215	6	US-10-953-349-13402	Sequence 13402, A
39	32	43.8	260	6	US-10-953-349-13883	Sequence 13883, A
40	32	43.8	290	6	US-10-953-349-5422	Sequence 5422, Ap
41	32	43.8	298	7	US-11-293-697-2712	Sequence 2712, Ap
42	32	43.8	312	7	US-11-140-450-81	Sequence 81, Appl
43	32	43.8	320	6	US-10-953-349-16365	Sequence 16365, A
44	32	43.8	363	6	US-10-953-349-16364	Sequence 16364, A
45 46	32	43.8	384	6	US-10-953-349-16363	Sequence 16363, A
47	32 32	43.8 43.8	426 513	6 6	US-10-953-349-5421 US-10-953-349-32711	Sequence 5421, Ap
48	32	43.8	529	7	US-11-223-945-34	Sequence 32711, A Sequence 34, Appl
49	32	43.8	531	6	US-10-953-349-5420	Sequence 54, Appl Sequence 5420, Ap
50	32	43.8	548	6	US-10-953-349-32710	Sequence 3420, Ap
51	32	43.8	576	6	US-10-953-349-32301	Sequence 32301, A
52	32	43.8	613	6	US-10-953-349-32709	Sequence 32709, A
53	32	43.8	648	7	US-11-024-544A-8	Sequence 8, Appli
54	32	43.8	648	7	US-11-190-750-60	Sequence 60, Appl
55	32	43.8	648	7	US-11-264-784-77	Sequence 77, Appl
56	32	43.8	648	7	US-11-264-737-118	Sequence 118, App
57	32	43.8	689	6	US-10-953-349-32300	Sequence 32300, A
58	32	43.8	695	7	US-11-258-767-26	Sequence 26, Appl
59	32	43.8	745	6	US-10-953-349-32299	Sequence 32299, A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-6.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 6.rai.

<u>start</u>

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OM protein - protein search, using sw model

June 2, 2006, 19:12:07; Search time 12.7 Seconds Run on:

(without alignments)

103.383 Million cell updates/sec

Title: US-10-001-938-6

Perfect score: 80

Sequence: 1 GDLYVQVQVKQHPIF 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

> 1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:* 4: /EMC Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:* 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:* 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	80	100.0	399		US-09-553-498-2	Sequence 2, Appli
2	80	100.0	399		US-09-618-869-2	Sequence 2, Appli

_				_		_	
3	72	90.0	380	2	US-09-489-039A-9011	Sequence	9011, Ap
4	63	78.8	380	2	US-09-543-681A-5912	Sequence	5912, Ap
5	62	77.5	376	3	US-10-375-010-22	Sequence	22, Appl
6	62	77.5	381	2	US-09-252-991A-27174	_	27174, A
7		76.2	209	2		-	Ī
	61			_	US-09-902-540-14118	-	14118, A
8	59	73.8	407	2	US-09-540-236-2899	Sequence	2899, Ap
9	56	70.0	375	2	US-09-328-352-4984	Sequence	4984, Ap
10	56	70.0	392	2	US-09-198-452A-48	Sequence	48, Appl
11	56	70.0	406	2	US-09-438-185A-34	•	34, Appl
				_		-	•
12	54	67.5	382	2	US-09-603-208A-40		40, Appl
13	52	65.0	391	2	US-09-902-540-11110	Sequence	11110, A
14	46	57.5	121	2	US-09-717-321A-29	Sequence	29, Appl
15	46	57.5	320	2	US-09-543-681A-7884	Seguence	7884, Ap
16	46	57.5	358	1	US-08-868-288A-1	-	1, Appli
17	46	57.5	358	2	US-09-235-373-1	_	1, Appli
18	46	57.5	358	2	US-09-388-993-1	Sequence	1, Appli
19	46	57.5	358	2	US-09-991-181-148	Sequence	148, App
20	46	57.5	358	2	US-09-501-714-1	Seguence	1, Appli
21	46	57.5	358	2	US-09-990-444-148		148, App
				_			
22	46	57.5	358	2	US-09-997-333-148	Sequence	
23	46	57.5	358	2	US-09-992-598-148	Sequence	148, App
24	46	57.5	358	2	US-09-989-735-148	Sequence	148, App
25	46	57.5	358	3	US-09-989-726-148	Sequence	
26	46	57.5	358	3	US-09-997-514-148	Sequence	
					· · - · · · · ·	-	• •
27	46	57.5	358	3	US-09-989-728-148		148, App
28	46	57.5	358	3	US-09-997-349-148	Sequence	148, App
29	46	57.5	358	3	US-09-997-653-148	Sequence	148, App
30	46	57.5	358	3	US-09-989-293A-148	-	148, App
31	45	56.2	368	2	US-09-861-451A-2		2, Appli
						-	
32	45	56.2	395	2	US-09-603-208A-28	_	28, Appl
33	44	55.0	286	2	US-09-902-540-11710	Sequence	11710, A
34	44	55.0	308	2	US-09-489-039A-8590	Sequence	8590, Ap
35	43	53.8	324	2	US-09-248-796A-15091	Sequence	15091, A
36	43	53.8	395	2	US-09-712-363-164	-	164, App
37						~	
	43	53.8	493	2	US-09-613-303-19	-	19, Appl
38	43	53.8	493	2	US-10-267-311-19	Sequence	19, Appl
39	41	51.2	286	2	US-09-902-540-11427	Sequence	11427, A
40	40.5	50.6	450	2	US-09-857-524B-8	Sequence	8, Appli
41	40	50.0	180	2	US-09-936-588-45	_	45, Appl
42				2		-	
	40	50.0	288		US-09-107-532A-7120	_	7120, Ap
43	40	50.0	320	2	US-09-328-352-7937	Sequence	7937, Ap
44	40	50.0	505	2	US-09-902-540-12326	Sequence	12326, A
45	40	50.0	579	2	US-09-489-039A-12334	Sequence	12334, A
46	40	50.0	608	2	US-09-310-275-2	•	2, Appli
47	40	50.0	608	2	US-09-082-077-5	-	5, Appli
48	40	50.0	608	2	US-09-925-637-70	-	70, Appl
49	39.5	49.4	680	2	US-09-248-796A-15089	Sequence	15089, A
50	39	48.8	65	2	US-09-910-009A-357	Sequence	357, App
51	38.5	48.1	446	1	US-08-833-610-5	Sequence	5, Appli
52	38.5	48.1	446	2	US-08-834-033A-15	-	15, Appl
						_	
53	38.5	48.1	446	2	US-09-377-452-5		5, Appli
54	38.5	48.1	447	2	US-09-555-093-7		7, Appli
55	38.5	48.1	448	1	US-08-366-779-5	Sequence	5, Appli
56	38.5	48.1	448	1	US-08-789-936-5	Sequence	5, Appli
57	38.5	48.1	448	2	US-08-934-254-5	•	5, Appli
58	38.5	48.1	448	2	US-09-685-775-5	-	5, Appli
				_			
59	38.5	48.1	448	2	US-09-857-583B-15	_	15, Appl
60	38.5	48.1	448	2	US-09-857-524B-11		11, Appl
61	38	47.5	67	2	US-09-910-009A-271	Sequence	271, App
62	38	47.5	129	2	US-09-621-976-4541	Sequence	4541, Ap
63	38	47.5	244	2	US-09-134-000C-4358	-	4358, Ap
- -	3.0	. , . •		_		204401100	,

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-6.ra

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 6.rapbm.

<u>start</u>

Go Back to pri

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:45:16; Search time 63.4 Seconds

(without alignments)

109.593 Million cell updates/sec

Title: US-10-001-938-6

Perfect score: 80

Sequence: 1 GDLYVQVQVKQHPIF 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database: Published_Applications_AA_Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	80	100.0	15	4	US-10-001-938-6	Sequence 6, Appli
2	80	100.0	341	3	US-09-764-868-1152	Sequence 1152, Ap
3	80	100.0	376	4	US-10-369-493-689	Sequence 689, App

4	0.0	100 0	276		*** 11 000 450 22	0	- 20 N1
4	80	100.0	376	6	US-11-080-458-32	_	e 32, Appl
5	74	92.5	340	3	US-09-764-868-1153	•	e 1153, Ap
6	70	87.5	378	4	US-10-369-493-8450	Sequenc	e 8450, Ap
7	67	83.8	362	4	US-10-369-493-9305	Sequenc	e 9305, Ap
8	65	81.2	161	5	US-10-450-763-55085	Sequenc	e 55085, A
9	65	81.2	378	4	US-10-369-493-386	Sequenc	ce 386, App
10	65	81.2	378	4	US-10-369-493-21305	Sequenc	e 21305, A
11	62	77.5	376	4	US-10-375-010-22	_	ce 22, Appl
12	62	77.5	376	6	US-11-232-406A-22	-	ce 22, Appl
13	61	76.2	379	4	US-10-369-493-7330	•	e 7330, Ap
		76.2	380	4	US-10-369-493-4573	-	
14	61			-		•	ce 4573, Ap
15	60	75.0	364	4	US-10-369-493-134	•	e 134, App
16	59	73.8	375	4	US-10-369-493-15859	•	e 15859, A
17	59	73.8	376	4	US-10-369-493-15487	•	e 15487, A
18	58	72.5	296	4	US-10-282-122A-61258	Sequenc	e 61258, A
19	56	70.0	392	4	US-10-289-762-48	Sequenc	ce 48, Appl
20	55	68.8	396	4	US-10-156-761-12020	Sequenc	ce 12020, A
21	54	67.5	330	4	US-10-369-493-19832	Sequenc	ce 19832, A
22	54	67.5	331	4	US-10-369-493-18770	Sequenc	ce 18770, A
23	54	67.5	376	4	US-10-369-493-1212	•	ce 1212, Ap
24	54	67.5	382	3	US-09-738-626-6012	•	e 6012, Ap
25	54	67.5	382	5	US-10-703-799B-40	_	ce 40, Appl
26	53	66.2	236	4	US-10-424-599-282285	_	ce 282285,
				•		_	
27	53	66.2	367	4	US-10-369-493-8095	•	e 8095, Ap
28	53	66.2	374	4	US-10-369-493-13658	-	e 13658, A
29	53	66.2	376	4	US-10-369-493-47	-	ce 47, Appl
30	53	66.2	384	4	US-10-369-493-21849	•	ce 21849, A
31	53	66.2	458	4	US-10-424-599-282290	-	ce 282290,
32	52	65.0	214	4	US-10-425-114-61777	Sequenc	ce 61777, A
33	52	65.0	239	6	US-11-096-568A-18418	Sequenc	ce 18418, A
34	52	65.0	266	6	US-11-096-568A-18417	Sequenc	ce 18417, A
35	52	65.0	344	5	US-10-467-657-8284	Sequenc	ce 8284, Ap
36	52	65.0	368	4	US-10-369-493-19421	Sequenc	ce 19421, A
37	52	65.0	419	4	US-10-437-963-201815	-	ce 201815,
38	52	65.0	429	4	US-10-425-115-209640	-	e 209640,
39	52	65.0	429	6	US-11-096-568A-18416	_	ce 18416, A
40	51	63.7	168	4	US-10-767-701-39210	•	ce 39210, A
41	51	63.7	307	4	US-10-369-493-2647	•	ce 2647, Ap
42		63.7		4		•	
	51		317	_	US-10-156-761-14768	-	ce 14768, A
43	51	63.7	369	4	US-10-369-493-19646	-	e 19646, A
44	51	63.7	382	4	US-10-369-493-8065	-	ce 8065, Ap
45	51	63.7	442	4	US-10-437-963-196211	•	ce 196211,
46	50	62.5	308	4	US-10-369-493-19014	•	ce 19014, A
47	50	62.5	332	4	US-10-369-493-2834	Sequenc	ce 2834, Ap
48	49	61.3	312	4	US-10-282-122A-50995	Sequenc	ce 50995, A
49	49	61.3	418	4	US-10-425-115-271144	Sequenc	ce 271144,
50	49	61.3	528	4	US-10-369-493-22651	Sequenc	ce 22651, A
51	48	60.0	350	4	US-10-369-493-21024	Sequenc	ce 21024, A
52	48	60.0	420	4	US-10-369-493-591	•	ce 591, App
53	47	58.8	310	4	US-10-369-493-4694	•	ce 4694, Ap
54	47	58.8	322	4	US-10-369-493-20073	•	ce 20073, A
55	47	58.8	329	4	US-10-282-122A-49700	•	ce 49700, A
					·	-	
56	47	58.8	358	4	US-10-369-493-9641	•	ce 9641, Ap
57	47	58.8	391	4	US-10-369-493-18560	-	ce 18560, A
58	46	57.5	61	4	US-10-424-599-255229	_	ce 255229,
59	46	57.5	289	4	US-10-458-143-20	•	ce 20, Appl
60	46	57.5	314	4	US-10-282-122A-69193	_	ce 69193, A
61	46	57.5	319	4	US-10-282-122A-69287	-	ce 69287, A
62	46	57.5	358	3	US-09-989-722-148	Sequen	ce 148, App
63	46	57.5	358	3	US-09-989-723-148	Sequenc	ce 148, App
64	46	57.5	358	3	US-09-989-279-148	Sequenc	ce 148, App
						_	

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-6.rapbn.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:44:08; Search time 3.1 Seconds

(without alignments)

55.960 Million cell updates/sec

Title:

US-10-001-938-6

Perfect score: 80

1 GDLYVQVQVKQHPIF 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

Sequence:

58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database:

Published Applications AA New:*

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 NEW PUB.pep:*

4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 NEW PUB.pep:*

5: /EMC Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10 NEW PUB.pep:*

7: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11 NEW_PUB.pep:*

8: /EMC Celerra SIDS3/ptodata/2/pubpaa/US60 NEW PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

ક

No.	Score	Match	Length	DB	ID	Description
1	80	100.0	15	6	US-10-490-949-7	Sequence 7, Appli
2	51	63.7	332	6	US-10-953-349-1407	Sequence 1407, Ap
3	51	63.7	367	6	US-10-953-349-1406	Sequence 1406, Ap
4	51	63.7	456	6	US-10-953-349-1405	Sequence 1405, Ap
5	43	53.8	338	6	US-10-953-349-13711	Sequence 13711, A
6	43	53.8	367	6	US-10-953-349-9124	Sequence 9124, Ap
7	43	53.8	382	6	US-10-953-349-13710	Sequence 13710, A
8	43	53.8	396	6	US-10-953-349-9123	Sequence 9123, Ap
9	43	53.8	406	6	US-10-953-349-9122	Sequence 9122, Ap
10	43	53.8	420	6	US-10-953-349-13709	Sequence 13709, A
11	41	51.2	257	6	US-10-953-349-1056	Sequence 1056, Ap
12	41	51.2	337	6	US-10-953-349-1055	Sequence 1055, Ap
13	41	51.2	419	6	US-10-953-349-1054	Sequence 1054, Ap
14	39	48.8	256	6	US-10-953-349-16379	Sequence 16379, A
15	39	48.8	336	6	US-10-953-349-16378	Sequence 16378, A
16	39	48.8	360	6	US-10-953-349-20603	Sequence 20603, A
17	39	48.8	389	6	US-10-953-349-20602	Sequence 20602, A
18	39	48.8	390	6	US-10-953-349-20601	Sequence 20601, A
19	39	48.8	402	6	US-10-953-349-4763	Sequence 4763, Ap
20	39	48.8	411	6	US-10-953-349-4762	Sequence 4762, Ap
21	39	48.8	415	6	US-10-953-349-4761	Sequence 4761, Ap
22	39	48.8	417	6	US-10-953-349-16377	Sequence 16377, A
23	38.5	48.1	448	6	US-10-975-692-15	Sequence 15, Appl
24	38	47.5	389	7	US-11-122-986-185	Sequence 185, App
25	38	47.5	389	7	US-11-122-986-187	Sequence 187, App
26	38	47.5	407	6	US-10-953-349-2666	Sequence 2666, Ap
27	38	47.5	443	6	US-10-953-349-2665	Sequence 2665, Ap
28	37.5	46.9	630	7	US-11-293-697-3776	Sequence 3776, Ap
29	36	45.0	380	6	US-10-953-349-7175	Sequence 7175, Ap
30	36	45.0	391	6	US-10-953-349-7174	Sequence 7174, Ap
31	36	45.0	408	6	US-10-953-349-17120	Sequence 17120, A
32	36	45.0	442	6	US-10-953-349-7173	Sequence 7173, Ap
33	36	45.0	587	6	US-10-953-349-17119	Sequence 17119, A
34	36	45.0	674	6	US-10-953-349-17118	Sequence 17118, A
35	36	45.0	706	6	US-10-511-937-2450	Sequence 2450, Ap
36 27	35	43.8	307	6	US-10-953-349-2183	Sequence 2183, Ap
37	35	43.8	335	6	US-10-953-349-2182	Sequence 2182, Ap
38	35	43.8	343	6	US-10-953-349-2181	Sequence 2181, Ap
39	34	42.5	188	6	US-10-953-349-2975	Sequence 2975, Ap
40	34	42.5	206	6	US-10-953-349-7113	Sequence 7113, Ap
41 42	34	42.5	216	6	US-10-953-349-2974	Sequence 2974, Ap
42	34 34	42.5 42.5	244 251	6 6	US-10-953-349-7112 US-10-953-349-29525	Sequence 7112, Ap
44	34	42.5	255	6	US-10-953-349-7111	Sequence 29525, A
45	34	42.5	275	6	US-10-953-349-7111	Sequence 7111, Ap
46	34	42.5	298	6	US-10-953-349-24595	Sequence 24596, A Sequence 24595, A
47	34	42.5	323	7	US-11-249-111-102	Sequence 102, App
48	34	42.5	345	6	US-10-511-937-2562	Sequence 2562, App
49	34	42.5	355	6	US-10-953-349-2973	Sequence 2973, Ap
50	34	42.5	398	6	US-10-953-349-20591	Sequence 20591, Ap
51	34	42.5	401	6	US-10-953-349-24594	Sequence 24594, A
52	34	42.5	415	6	US-10-953-349-20590	Sequence 20590, A
53	34	42.5	419	6	US-10-953-349-20589	Sequence 20589, A
54	34	42.5	580	6	US-10-953-349-24438	Sequence 24438, A
55	34	42.5	635	6	US-10-953-349-24437	Sequence 24437, A
56	34	42.5	636	6	US-10-953-349-24436	Sequence 24436, A
57	33	41.2	138	6	US-10-542-038-17	Sequence 17, Appl
58	33	41.2	159	6	US-10-542-038-4	Sequence 4, Appli
59	33	41.2	358	6	US-10-953-349-32194	Sequence 32194, A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-7.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 7.rai.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

June 2, 2006, 19:08:52; Search time 11.4238 Seconds Run on:

(without alignments)

114.932 Million cell updates/sec

US-10-001-938-7 Title:

Perfect score: 81

Sequence: 1 YCEVPINFAMAALGG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

650591 seqs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters: 650591

Minimum DB seg length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:* 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:* 4: /EMC Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:* 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:* /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	81	100.0	399	2	US-09-553-498-2	Sequence 2, Appli
2	81	100.0	399	2	US-09-618-869-2	Sequence 2, Appli

3	77	95.1	380	2	US-09-543-681A-5912	Sequence	5912, Ap
4	77	95.1	380	2	US-09-489-039A-9011	Sequence	9011, Ap
5	68	84.0	381	2	US-09-252-991A-27174	Sequence	27174, A
6	59	72.8	376	3	US-10-375-010-22	Sequence	22, Appl
7	57	70.4	209	2	US-09-902-540-14118	Sequence	14118, A
8	45	55.6	288	2	US-09-107-532A-7120	•	7120, Ap
9	43	53.1	244	2	US-09-134-000C-4358		4358, Ap
10	42	51.9	375	2	US-09-328-352-4984	-	4984, Ap
11	42	51.9	417	2	US-09-489-039A-7357	-	7357, Ap
						-	•
12	41	50.6	274	2	US-09-248-796A-20766	-	20766, A
13	41	50.6	280	2	US-09-248-796A-20765	•	20765, A
14	41	50.6	648	2	US-09-538-092-536	-	536, App
15	39	48.1	127	2	US-09-198-452A-359	Sequence	359, App
16	39	48.1	148	2	US-09-438-185A-344	Sequence	344, App
17	39	48.1	244	2	US-09-198-452A-360	Sequence	360, App
18	39	48.1	256	2	US-09-270-767-33692	Sequence	33692, A
19	39	48.1	256	2	US-09-270-767-48909	•	48909, A
20	39	48.1	324	2	US-09-902-540-12246	•	12246, A
21	39	48.1	369	2	US-09-252-991A-18429	•	18429, A
22	39	48.1	370	2	US-09-377-285B-16	-	16, Appl
				_		-	• •
23	39	48.1	370	2	US-10-192-381-16		16, Appl
24	39	48.1	720	2	US-09-328-352-4435	<u>-</u>	4435, Ap
25	39	48.1	1058	1	US-08-247-904B-14	-	14, Appl
26	39	48.1	1058	2	US-08-767-942A-15	Sequence	15, Appl
27	39	48.1	1058	2	US-09-826-312A-2	Sequence	2, Appli
28	39	48.1	1058	2	US-09-538-092-985	Sequence	985, App
29	39	48.1	1058	3	US-10-835-096-2	Sequence	2, Appli
30	39	48.1	1059	2	US-09-542-497A-2	-	2, Appli
31	39	48.1	1059	2	US-10-108-767-2	•	2, Appli
32	39	48.1	1059	2	US-10-152-156-2	-	2, Appli
33	38	46.9	85	1	US-08-480-229C-7	_	7, Appli
34	38	46.9	85	1	US-08-659-235C-7	•	
						•	7, Appli
35	38	46.9	104	1	US-08-111-939-26	-	26, Appl
36	38	46.9	108	1	US-08-162-402B-27	-	27, Appl
37	38	46.9	318	2	US-09-902-540-15648	-	15648, A
38	38	46.9	363	2	US-09-489-039A-13446	•	13446, A
39	38	46.9	392	2	US-09-198-452A-48	•	48, Appl
40	38	46.9	395	2	US-09-603-208A-28	Sequence	28, Appl
41	38	46.9	406	2	US-09-438-185A-34	Sequence	34, Appl
42	37	45.7	115	1	US-08-152-922A-7	Sequence	7, Appli
43	37	45.7	158	2	US-09-270-767-35277	_	35277, A
44	37	45.7	158	2	US-09-270-767-50494	-	50494, A
45	37	45.7	334	2	US-09-546-986A-8	•	8, Appli
46	37	45.7	334	2	US-09-524-730-8	_	8, Appli
47	37	45.7	427	2	US-09-489-039A-8493	•	8493, Ap
48	37	45.7	502	2	US-09-134-000C-6611	-	6611, Ap
						-	· · · · · · · · · · · · · · · · · · ·
49	37	45.7	767 701	2	US-09-540-236-2346	-	2346, Ap
50	37	45.7	781	2	US-10-094-749-2636	-	2636, Ap
51	37	45.7	861	2	US-09-949-016-11001	•	11001, A
52	37	45.7	1285	1	US-07-582-945-2	Sequence	2, Appli
53	37	45.7	1285	1	US-08-453-141-2	Sequence	2, Appli
54	37	45.7	1285	2	US-08-293-314-2	Sequence	2, Appli
55	37	45.7	1602	2	US-09-269-874A-7	Sequence	7, Appli
56	37	45.7	1621	2	US-09-269-874A-5	Sequence	5, Appli
57	37	45.7	1639	2	US-09-269-874A-3	-	3, Appli
58	36	44.4	183	2	US-09-252-991A-26190	-	26190, A
59	36	44.4	196	2	US-09-270-767-45964	-	45964, A
60	36	44.4	217	2	US-09-328-352-5479	•	5479, Ap
61	36	44.4	251	2	US-09-663-600A-99	-	99, Appl
62						-	
	36 36	44.4	251	2	US-09-663-600A-193	_	193, App
63	36	44.4	358	2	US-09-134-001C-5461	sequence	5461, Ap

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-7.ra

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-007. This page gives you Search Results detail for the Application 10001938 and Search Result us-10-007.

start

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2006, 19:29:53; Search time 75.9934 Seconds

(without alignments)

91.432 Million cell updates/sec

Title: US-10-001-938-7

Perfect score: 81

Sequence: 1 YCEVPINFAMAALGG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database: Published_Applications_AA_Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	81	100.0	15	4	US-10-001-938-7	Sequence 7, Appli
2	81	100.0	161	5	US-10-450-763-55085	Sequence 55085, A
3	81	100.0	340	3	US-09-764-868-1153	Sequence 1153, Ap

		_		_	_		
4	81	100.0	341	3	US-09-764-868-1152	Sequence	1152, Ap
5	81	100.0	376	4	US-10-369-493-689	Sequence	689, App
6	81	100.0	376	6	US-11-080-458-32	Sequence	32, Appl
7	75	92.6	378	4	US-10-369-493-386	•	386, App
8	75	92.6	378	4	US-10-369-493-21305	•	21305, A
9	68	84.0	344	5	US-10-467-657-8284	•	8284, Ap
						-	•
10	62	76.5	369	4	US-10-369-493-19646	-	19646, A
11	60	74.1	374	4	US-10-369-493-13658	•	13658, A
12	59	72.8	358	4	US-10-369-493-9641	Sequence	9641, Ap
13	59	72.8	372	4	US-10-369-493-23206	Sequence	23206, A
14	59	72.8	376	4	US-10-375-010-22	Sequence	22, Appl
15	59	72.8	376	6	US-11-232-406A-22	_	22, Appl
16	59	72.8	378	4	US-10-369-493-8450	•	8450, Ap
17	56	69.1	15	4	US-10-001-938-8	•	8, Appli
				_		•	• •
18	56	69.1	376	4	US-10-369-493-12087	•	12087, A
19	54	66.7	382	4	US-10-369-493-8065	-	8065, Ap
20	52	64.2	379	4	US-10-369-493-7330	Sequence	7330, Ap
21	52	64.2	380	4	US-10-369-493-4573	Sequence	4573, Ap
22	51	63.0	370	4	US-10-369-493-17209	Sequence	17209, A
23	51	63.0	384	6	US-11-074-176-78	-	78, Appl
24	50	61.7	375	4	US-10-369-493-15859	-	15859, A
25	50	61.7	376	4		•	•
				_	US-10-369-493-15487	•	15487, A
26	50	61.7	384	4	US-10-369-493-21849	-	21849, A
27	49	60.5	362	4	US-10-369-493-9305	•	9305, Ap
28	46	56.8	377	6	US-11-045-004-1504	Sequence	1504, Ap
29	46	56.8	396	4	US-10-156-761-12020	Sequence	12020, A
30	45	55.6	376	4	US-10-369-493-1212	Sequence	1212, Ap
31	45	55.6	467	4	US-10-074-978A-247	•	247, App
32	44	54.3	364	6	US-11-087-099-10854	_	10854, A
33	43	53.1	152	4	US-10-767-701-51964	•	51964, A
34				5		-	•
	43	53.1	271	_	US-10-506-454-953	-	953, App
35	43	53.1	331	4	US-10-369-493-18770	•	18770, A
36	43	53.1	385	4	US-10-369-493-16754	•	16754, A
37	42	51.9	123	3	US-09-764-877-1594	Sequence	1594, Ap
38	42	51.9	123	4	US-10-242-515-1594	Sequence	1594, Ap
39	42	51.9	196	5	US-10-450-763-57058	Sequence	57058, A
40	42	51.9	295	5	US-10-450-763-57057	Sequence	57057, A
41	42	51.9	403	5	US-10-732-923-23825	_	23825, A
42	42	51.9	418	5	US-10-732-923-23808	•	23808, A
43	42	51.9	418	5	US-10-732-923-23829	•	23829, A
				_		-	·
44	42	51.9	428	5	US-10-450-763-48608	-	48608, A
45	41	50.6	168	4	US-10-437-963-138551	Sequence	•
46	41	50.6	365	4	US-10-369-493-10648	•	10648, A
47	41	50.6	648	4	US-10-149-310-116	Sequence	116, App
48	41	50.6	759	4	US-10-149-310-218	Sequence	218, App
49	40	49.4	194	4	US-10-767-701-55799	Sequence	55799, A
50	40	49.4	241	6	US-11-188-298-6441		6441, Ap
51	40	49.4	330	4	US-10-369-493-19832	•	19832, A
52	40	49.4	345	4	US-10-282-122A-74172	•	74172, A
53	40	49.4	345	4	US-10-474-776-387	•	•
				_		_	387, App
54	40	49.4	345	5	US-10-472-928-4098	•	4098, Ap
55	40	49.4	379	4	US-10-369-493-18523	•	18523, A
56	40	49.4	413	5	US-10-732-923-23809	Sequence	23809, A
57	39.5	48.8	416	6	US-11-188-298-349	Sequence	349, App
58	39.5	48.8	1902	4	US-10-437-963-139559	Sequence	139559,
59	39	48.1	110	4	US-10-425-115-265773	Sequence	265773,
60	39	48.1	127	4	US-10-289-762-359	•	359, App
61	39	48.1	148	4	US-10-767-701-51826	-	51826, A
62	39	48.1	166	4	US-10-424-599-181463	Sequence	·
63	39	48.1	170	4	US-10-424-333-181403 US-10-425-115-265740	Sequence	•
				_		-	•
64	39	48.1	205	5	US-10-450-763-53421	sequence	53421, A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-7.rapbn.

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Go Back to previous pa

GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:30:30; Search time 3.57616 Seconds

(without alignments)

48.509 Million cell updates/sec

Title:

US-10-001-938-7

Perfect score: 81

Sequence: 1 YCEVPINFAMAALGG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

58871 segs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08 NEW PUB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

No.	Score	Match	Length	DB	ID	Description
1	81	100.0	15	6	US-10-490-949-8	Sequence 8, Appli
2	56	69.1	15	6	US-10-490-949-9	Sequence 9, Appli
3	43	53.1	389	7	US-11-122-986-185	Sequence 185, App
4	43	53.1	389	7	US-11-122-986-187	Sequence 187, App
5	39	48.1	177	6	US-10-953-349-40074	Sequence 40074, A
6	39	48.1	1058	7	US-11-251-673-3	Sequence 3, Appli
7	39	48.1	1058	7	US-11-328-747-2	Sequence 2, Appli
8 9	38 38	46.9 46.9	264 299	6 6	US-10-953-349-31925 US-10-953-349-31924	Sequence 31925, A Sequence 31924, A
10	38	46.9	341	6	US-10-953-349-31923	Sequence 31923, A
11	36	44.4	337	6	US-10-953-349-34607	Sequence 34607, A
12	36	44.4	381	6	US-10-953-349-34606	Sequence 34606, A
13	35	43.2	20	7	US-11-301-554-1837	Sequence 1837, Ap
14	35	43.2	20	7	US-11-301-554-1838	Sequence 1838, Ap
15	35	43.2	200	7	US-11-301-554-324	Sequence 324, App
16	35	43.2	200	7	US-11-301-554-789	Sequence 789, App
17	35	43.2	207	7	US-11-301-554-1667	Sequence 1667, Ap
18	35	43.2	207	7	US-11-301-554-1913	Sequence 1913, Ap
19	35	43.2	468	6	US-10-953-349-13528	Sequence 13528, A
20	35	43.2	516	6	US-10-953-349-5638	Sequence 5638, Ap
21	35	43.2	543	6	US-10-953-349-5637	Sequence 5637, Ap
22	35	43.2	558	6	US-10-953-349-5636	Sequence 5636, Ap
23	35	43.2	589	6	US-10-953-349-13527	Sequence 13527, A
24 25	35 34.5	43.2 42.6	620 125	6 6	US-10-953-349-13526 US-10-953-349-31810	Sequence 13526, A Sequence 31810, A
25 26	34.3	42.0	134	6	US-10-953-349-25326	Sequence 25326, A
27	34	42.0	178	6	US-10-953-349-32321	Sequence 32321, A
28	34	42.0	188	6	US-10-953-349-32320	Sequence 32320, A
29	34	42.0	215	6	US-10-953-349-32319	Sequence 32319, A
30	34	42.0	269	6	US-10-953-349-35364	Sequence 35364, A
31	34	42.0	276	6	US-10-953-349-35363	Sequence 35363, A
32	34	42.0	279	6	US-10-953-349-35362	Sequence 35362, A
33	34	42.0	654	7	US-11-121-154-191	Sequence 191, App
34	34	42.0	677	7	US-11-293-697-4521	Sequence 4521, Ap
35	33	40.7	14	7	US-11-122-986-191	Sequence 191, App
36	33	40.7	236	6	US-10-953-349-2804	Sequence 2804, Ap
37	33	40.7	241	6	US-10-953-349-23181	Sequence 23181, A
38	33	40.7	247	6	US-10-953-349-23180	Sequence 23180, A
39	33	40.7	337	6	US-10-953-349-13157	Sequence 13157, A
40 41	33 33	40.7 40.7	387 396	6 7	US-10-953-349-13156 US-11-293-697-4386	Sequence 13156, A Sequence 4386, Ap
42	33	40.7	423	6	US-10-953-349-2803	Sequence 2803, Ap
43	33	40.7	425	6	US-10-953-349-15552	Sequence 15552, A
44	33	40.7	429	6	US-10-953-349-2802	Sequence 2802, Ap
45	33	40.7	443	6	US-10-953-349-17462	Sequence 17462, A
46	33	40.7	485	6	US-10-953-349-13155	Sequence 13155, A
47	33	40.7	547	7	US-11-293-697-2751	Sequence 2751, Ap
48	33	40.7	589	7	US-11-311-778-6	Sequence 6, Appli
49	33	40.7	640	7	US-11-311-778-4	Sequence 4, Appli
50	33	40.7	800	7	US-11-293-697-2490	Sequence 2490, Ap
51	33	40.7	1178	7	US-11-311-778-10	Sequence 10, Appl
52	33	40.7	1178	7	US-11-311-778-12	Sequence 12, Appl
53	33	40.7	1178	7	US-11-311-778-14	Sequence 14, Appl
54 55	32	39.5	252	6	US-10-953-349-8893	Sequence 8893, Ap
55 56	32 32	39.5 39.5	253 294	6 6	US-10-953-349-8892 US-10-953-349-23218	Sequence 8892, Ap Sequence 23218, A
57	32	39.5	302	6	US-10-953-349-23216 US-10-953-349-8891	Sequence 8891, Ap
58	32	39.5	312	6	US-10-953-349-23217	Sequence 23217, Ap
59	32	39.5	316	6	US-10-953-349-23216	Sequence 23216, A
		• •	- 	-		1

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-8.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 8.rai.

start

Go Back to p

GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

June 2, 2006, 19:12:07; Search time 12.7 Seconds Run on:

(without alignments)

103.383 Million cell updates/sec

Title: US-10-001-938-8

Perfect score: 74

Sequence: 1 PINFAMAALGGEIEV 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

650591 seqs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Issued Patents AA:* Database :

> 1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:* 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:* 3: /EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:* 4: /EMC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:* 5: /EMC Celerra SIDS3/ptodata/2/iaa/PCTUS COMB.pep:*

> 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:* /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description		
1 2		100.0			US-09-553-498-2 US-09-618-869-2	Sequence 2, Appli Sequence 2, Appli		

3	70	94.6	380	2	US-09-543-681A-5912	Sequence	5912, Ap
4	70	94.6	380	2	US-09-489-039A-9011	Sequence	9011, Ap
5	60	81.1	376	3	US-10-375-010-22	Sequence	22, Appl
6	59	79.7	381	2	US-09-252-991A-27174	Sequence	27174, A
7	47	63.5	209	2	US-09-902-540-14118	-	14118, A
8	47	63.5	288	2	US-09-107-532A-7120	-	7120, Ap
9	45	60.8	244	2	US-09-134-000C-4358	•	4358, Ap
10	45	60.8	375	2	US-09-328-352-4984	•	4984, Ap
						•	_
11	44	59.5	407	2	US-09-540-236-2899	•	2899, Ap
12	42	56.8	373	2	US-09-710-279-890	-	890, App
13	42	56.8	385	2	US-09-134-001C-3688	-	3688, Ap
14	42	56.8	395	2	US-09-603-208A-28	•	28, Appl
15	41	55.4	274	2	US-09-248-796A-20766	Sequence	20766, A
16	41	55.4	280	2	US-09-248-796A-20765	Sequence	20765, A
17	40	54.1	253	2	US-08-975-762-52	Sequence	52, Appl
18	40	54.1	253	2	US-09-295-028-52	Sequence	52, Appl
19	40	54.1	253	2	US-09-106-582-52	Sequence	
20	40	54.1	253	2	US-09-159-469-52	Sequence	
21	40	54.1	253	2	US-09-693-542-52	Sequence	
22	40	54.1	326	2	US-09-066-046-29	-	29, Appl
23	40	54.1	326	2	US-09-066-047-15	-	15, Appl
				_		-	
24	40	54.1	425	2	US-09-288-339-4	-	4, Appli
25	40	54.1	435	2	US-09-066-046-27	_	27, Appl
26	40	54.1	435	2	US-09-066-047-13	_	13, Appl
27	39.5	53.4	538	2	US-09-107-532A-5563	-	5563, Ap
28	39	52.7	324	2	US-09-902-540-12246	Sequence	12246, A
29	38	51.4	352	1	US-08-472-534-6	Sequence	6, Appli
30	38	51.4	378	2	US-09-583-110-4647	Sequence	4647, Ap
31	38	51.4	379	2	US-09-107-433-3487	Sequence	3487, Ap
32	38	51.4	532	2	US-09-252-991A-21005	Sequence	21005, A
33	37	50.0	34	1	US-08-118-270-190	Sequence	190, App
34	37	50.0	34	5	PCT-US93-08528-190		190, App
35	37	50.0	127	2	US-09-198-452A-359	-	359, App
36	37	50.0	148	2	US-09-438-185A-344	_	344, App
37	37	50.0	244	2	US-09-198-452A-360	-	360, App
38	37	50.0	321	2	US-09-498-520A-18	-	18, Appl
39	37	50.0	394	2	US-09-252-991A-22328	•	22328, A
				_		•	·
40	37	50.0	413	1	US-08-282-197C-49	₹	49, Appl
41	37	50.0	1319	2	US-09-538-092-1291	-	1291, Ap
42	37	50.0	1343	2	US-09-949-016-10641	-	10641, A
43	36	48.6	35	1	US-08-118-270-191	<u>=</u>	191, App
44	36	48.6	35	5	PCT-US93-08528-191	-	191, App
45	36	48.6	82	2	US-09-144-776B-18	Sequence	18, Appl
46	36	48.6	82	2	US-08-882-431B-18	Sequence	18, Appl
47	36	48.6	121	2	US-09-252-991A-19703	Sequence	19703, A
48	36	48.6	199	2	US-10-360-101-216	Sequence	216, App
49	36	48.6	228	2	US-08-896-933-25	Sequence	25, Appl
50	36	48.6	228	2	US-09-314-235-25	Sequence	25, Appl
51	36	48.6	228	2	US-09-708-008B-25	_	25, Appl
52	36	48.6	251	2	US-09-663-600A-99	-	99, Appl
53	36	48.6	251	2	US-09-663-600A-193	•	193, App
54	36	48.6	315	2	US-09-603-208A-212	~	212, App
55	36	48.6		2	US-09-252-991A-28744	_	28744, A
			327 361	_	US-09-583-110-2683	•	
56	36 36	48.6	361	2		-	2683, Ap
57	36	48.6	363	2	US-09-107-433-3946		3946, Ap
58	36	48.6	369	2	US-09-252-991A-18429	-	18429, A
59	36	48.6	432	2	US-09-118-319-2	-	2, Appli
60	36	48.6	464	2	US-09-252-991A-20795	•	20795, A
61	36	48.6	473	2	US-09-252-991A-23441	•	23441, A
62	36	48.6	483	2	US-09-603-208A-210	-	210, App
63	36	48.6	657	2	US-09-252-991A-23156	Sequence	23156, A

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-8.ra

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 8.rapbm.

start

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:45:16; Search time 63.4 Seconds

(without alignments)

109.593 Million cell updates/sec

Title: US-10-001-938-8

Perfect score: 74

Sequence: 1 PINFAMAALGGEIEV 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database: Published_Applications_AA_Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11 PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
1	74	100.0	15	4	US-10-001-938-8	Sequence 8, Appli
2	74	100.0	161	5	US-10-450-763-55085	Sequence 55085, A
3	74	100.0	340	3	US-09-764-868-1153	Sequence 1153, Ap

4	74	100.0	341	3	US-09-764-868-1152	Coguenge	1152 75
5	74	100.0	376	4	US-10-369-493-689	-	1152, Ap
6				_		_	689, App
7	74	100.0	376	6	US-11-080-458-32	_	32, Appl
	68	91.9	378	4	US-10-369-493-386	-	386, App
8	68	91.9	378	4	US-10-369-493-21305	•	21305, A
9	67	90.5	344	5	US-10-467-657-8284	•	8284, Ap
10	61	82.4	369	4	US-10-369-493-19646	-	19646, A
11	60	81.1	376	4	US-10-375-010-22	•	22, Appl
12	60	81.1	376	6	US-11-232-406A-22	_	22, Appl
13	60	81.1	378	4	US-10-369-493-8450	Sequence	8450, Ap
14	58	78.4	365	4	US-10-369-493-10648	Sequence	10648, A
15	56	75.7	15	4	US-10-001-938-7	Sequence	7, Appli
16	56	75.7	379	4	US-10-369-493-7330	Sequence	7330, Ap
17	56	75.7	380	4	US-10-369-493-4573	Sequence	4573, Ap
18	55	74.3	382	4	US-10-369-493-8065	Sequence	8065, Ap
19	55	74.3	396	4	US-10-156-761-12020	Sequence	12020, A
20	54	73.0	374	4	US-10-369-493-13658	Sequence	13658, A
21	53	71.6	372	4	US-10-369-493-23206	Sequence	•
22	51	68.9	384	4	US-10-369-493-21849	•	21849, A
23	50	67.6	379	4	US-10-369-493-18523	Sequence	•
24	49	66.2	365	4	US-10-369-493-18240	Sequence	•
25	48	64.9	358	4	US-10-369-493-9641	•	9641, Ap
26	47	63.5	384	6	US-11-074-176-78	-	78, Appl
27	47	63.5	420	4	US-10-369-493-591	=	591, App
28	46	62.2	370	4	US-10-369-493-17209	•	
				_		_	17209, A
29	46	62.2	376	4	US-10-369-493-1212	-	1212, Ap
30	45	60.8	377	6	US-11-045-004-1504	-	1504, Ap
31	44	59.5	354	4	US-10-369-493-11087	-	11087, A
32	44	59.5	376	4	US-10-369-493-12087	•	12087, A
33	43.5	58.8	271	5	US-10-506-454-953	•	953, App
34	43	58.1	256	4	US-10-424-599-248436	Sequence	
35	43	58.1	274	4	US-10-425-115-253738	Sequence	
36	43	58.1	1316	4	US-10-437-963-143011	Sequence	•
37	42	56.8	114	4	US-10-437-963-113572	Sequence	•
38	42	56.8	118	4	US-10-424-599-195865	Sequence	•
39	42	56.8	365	4	US-10-369-493-13503	Sequence	13503, A
40	42	56.8	373	5	US-10-793-626-890	Sequence	890, App
41	42	56.8	385	4	US-10-369-493-16754	Sequence	16754, A
42	42	56.8	395	3	US-09-738-626-6574	Sequence	6574, Ap
43	42	56.8	395	5	US-10-703-799B-28	Sequence	28, Appl
44	42	56.8	665	6	US-11-097-143-19728	Sequence	19728, A
45	41	55.4	398	6	US-11-098-686-11398	Sequence	11398, A
46	40	54.1	177	4	US-10-425-114-39492	Sequence	39492, A
47	40	54.1	253	3	US-09-159-469-52	Sequence	52, Appl
48	40	54.1	253	3	US-09-798-042-52	Sequence	52, Appl
49	40	54.1	253	3	US-09-953-108-52	-	52, Appl
50	40	54.1	330	5	US-10-732-923-13089	•	13089, A
51	40	54.1	424	4	US-10-437-963-192231	Sequence	*
52	40	54.1	425	4	US-10-223-598-4	-	4, Appli
53	40	54.1	587	4	US-10-425-114-73019	-	73019, A
54	40	54.1	724	4	US-10-437-963-121905	Sequence	•
55	39.5	53.4	519	4	US-10-282-122A-57987	•	57987, A
56	39	52.7	163	4	US-10-437-963-196051	Sequence	
57	39	52.7	385	5	US-10-501-282-4398	•	4398, Ap
58	39	52.7	395	6	US-11-079-463-9803	-	9803, Ap
59	39	52.7	471	4	US-10-369-493-5554	-	5554, Ap
60	39	52.7	471	4	US-10-369-493-5555	-	5555, Ap
61	38	51.4	142	4	US-10-767-701-39309	-	39309, A
62			208	4		-	•
	38	51.4			US-10-425-114-67304	-	67304, A
63 64	38	51.4	238	4	US-10-156-761-9379	•	9379, Ap
64	38	51.4	239	4	US-10-425-115-270985	Sequence	410303,

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-8.rapbn.

Score HomeRetrieve ApplicationSCORE SystemSCOREPageListOverviewFAQ

Comments / Suggestions

This page gives you Search Results detail for the Application 10001938 and Search Result us-10-001-938-8.rapbn.

start

Go Back to previous pag

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OM protein - protein search, using sw model

Run on: June 2, 2006, 19:44:08; Search time 3.1 Seconds

(without alignments)

55.960 Million cell updates/sec

Title: US-10-001-938-8

Perfect score: 74

Sequence: 1 PINFAMAALGGEIEV 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 58871 segs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database: Published Applications AA New:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08 NEW PUB.pep:*

5: /EMC Celerra SIDS3/ptodata/2/pubpaa/PCT NEW PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

7: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11 NEW_PUB.pep:*

8: /EMC Celerra SIDS3/ptodata/2/pubpaa/US60 NEW PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

ક

No.	Score	Match	Length	DB	ID	Description
1	74	100.0	15	6	US-10-490-949-9	Sequence 9, Appli
2	56	75.7	15	6	US-10-490-949-8	Sequence 8, Appli
3	45	60.8	389	7	US-11-122-986-185	Sequence 185, App
4	45	60.8	389	7	US-11-122-986-187	Sequence 187, App
5	37	50.0	467	6	US-10-953-349-32451	Sequence 32451, A
6	37	50.0	519	6	US-10-953-349-32450	Sequence 32450, A
7	37	50.0	521	6	US-10-953-349-32449	Sequence 32449, A
8	36	48.6	201	6	US-10-953-349-34141	Sequence 34141, A
9	36	48.6	207	6	US-10-953-349-34140	Sequence 34140, A
10	36	48.6	260	6	US-10-953-349-34139	Sequence 34139, A
11	35	47.3	368	6	US-10-953-349-7589	Sequence 7589, Ap
12	35	47.3	391	6	US-10-953-349-7588	Sequence 7588, Ap
13	35	47.3	438	6	US-10-953-349-7587	Sequence 7587, Ap
14	35	47.3	516	6	US-10-953-349-5638	Sequence 5638, Ap
15	35	47.3	543	6	US-10-953-349-5637	Sequence 5637, Ap
16	35	47.3	558	6	US-10-953-349-5636	Sequence 5636, Ap
17	34.5	46.6	312	7	US-11-140-450-81	Sequence 81, Appl
18	34	45.9	112	6	US-10-953-349-7574	Sequence 7574, Ap
19	34	45.9	249	6	US-10-953-349-14125	Sequence 14125, A
20	34	45.9	266	6	US-10-953-349-14124	Sequence 14124, A
21	34	45.9	382	6	US-10-953-349-14123	Sequence 14123, A
22	34	45.9	396	7	US-11-293-697-4386	Sequence 4386, Ap
23	34	45.9	677	7	US-11-293-697-4521	Sequence 4521, Ap
24	34	45.9	1049	7	US-11-251-340-23	Sequence 23, Appl
25	34	45.9	1058	7	US-11-251-673-3	Sequence 3, Appli
26	34	45.9	1058	7	US-11-328-747-2	Sequence 2, Appli
27	33	44.6	193	7 7	US-11-301-951-2	Sequence 2, Appli
28 29	33 33	44.6 44.6	193 193	7	US-11-301-951-4 US-11-301-951-6	Sequence 4, Appli Sequence 6, Appli
30	33	44.6	193	7	US-11-301-951-8	Sequence 8, Appli
31	33	44.6	217	6	US-10-953-349-18535	Sequence 18535, A
32	33	44.6	283	6	US-10-953-349-18534	Sequence 18534, A
33	33	44.6	307	6	US-10-953-349-18533	Sequence 18533, A
34	33	44.6	335	6	US-10-953-349-13374	Sequence 13374, A
35	33	44.6	339	6	US-10-953-349-13373	Sequence 13373, A
36	33	44.6		6	US-10-953-349-13372	Sequence 13372, A
37	33	44.6	425	6	US-10-953-349-15552	Sequence 15552, A
38	33	44.6	544	6	US-10-953-349-28426	Sequence 28426, A
39	33	44.6	788	7	US-11-121-154-47	Sequence 47, Appl
40	33	44.6	1912	6	US-10-511-937-2561	Sequence 2561, Ap
41	32.5	43.9	654	7	US-11-121-154-191	Sequence 191, App
42	32	43.2	122	6	US-10-953-349-5458	Sequence 5458, Ap
43	32	43.2	161	6	US-10-953-349-33744	Sequence 33744, A
44	32	43.2	174	6	US-10-953-349-5457	Sequence 5457, Ap
45	32	43.2	174	6	US-10-953-349-39794	Sequence 39794, A
46	32	43.2	278	6	US-10-953-349-30456	Sequence 30456, A
47	32	43.2	302	7	US-11-293-697-2615	Sequence 2615, Ap
48	32	43.2	350	6	US-10-522-043-8	Sequence 8, Appli
49	32	43.2	862	6	US-10-199-229-14	Sequence 14, Appl
50	32	43.2	875	6	US-10-199-229-10	Sequence 10, Appl
51	32	43.2	951	6	US-10-199-229-9	Sequence 9, Appli
52	32	43.2	951	6	US-10-199-229-13	Sequence 13, Appl
53	32	43.2	3113		US-10-505-928-325	Sequence 325, App
54	31.5	42.6	109	_	US-11-293-697-2786	Sequence 2786, Ap
55	31	41.9	172	6	US-10-953-349-37272	Sequence 37272, A
56	31	41.9	178	6	US-10-953-349-29145	Sequence 29145, A
57	31	41.9	182	6	US-10-953-349-1326	Sequence 1326, Ap
58	31	41.9	189	6	US-10-953-349-25147	Sequence 25147, A
59	31	41.9	206	6	US-10-953-349-1325	Sequence 1325, Ap

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-9.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 9.rai.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2006, 19:37:25; Search time 14.6053 Seconds

(without alignments)

89.896 Million cell updates/sec

Title: US-10-001-938-9

Perfect score: 73

Sequence: 1 ASYYEILDVPRSASA 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1 2	73 73	100.0 100.0	277 277	1 2		Sequence 7, Appli Sequence 7, Appli

2	7.0	100 0	0.55	•	00 200 002 7		
3	73	100.0	277	2	US-09-388-993-7	Sequence 7	·
4	73	100.0	277	2	US-09-501-714-7	Sequence 7	
5	73	100.0	327	2	US-09-949-016-11262	Sequence 1	-
6	73	100.0	351	1	US-08-868-288A-6	Sequence 6	
7	73	100.0	351	2	US-09-235-373-6	Sequence 6	
8	73	100.0	351	2	US-09-388-993-6	Sequence 6	o, Appli
9	73	100.0	351	2	US-09-501-714-6	Sequence 6	5, Appli
10	52	71.2	96	2	US-09-621-976-4045	Sequence 4	1045, Ap
11	52	71.2	223	2	US-09-658-644-4	Sequence 4	l, Appli
12	52	71.2	223	2	US-09-949-016-6832	Sequence 6	832, Ap
13	52	71.2	267	2	US-09-949-016-11497	Sequence 1	1497, A
14	51	69.9	419	1	US-08-686-417-3	Sequence 3	3, Appli
15	48	65.8	286	2	US-09-248-796A-16992	Sequence 1	.6992, A
16	48	65.8	387	2	US-09-908-992B-11	Sequence 1	1, Appl
17	48	65.8	414	2	US-09-908-992B-10	Sequence 1	0, Appl
18	48	65.8	452	2	US-09-908-992B-29	Sequence 2	
19	48	65.8	453	2	US-09-908-992B-9	Sequence 9	
20	48	65.8	453	2	US-09-908-992B-30	Sequence 3	·
21	48	65.8	479	2	US-09-908-992B-28	Sequence 2	
22	48	65.8	480	2	US-09-908-992B-8	Sequence 8	
23	48	65.8	480	2	US-09-908-992B-12	Sequence 1	
24	46	63.0	358	1	US-08-868-288A-1	Sequence 1	
25	46	63.0	358	2	US-09-235-373-1		
26	46	63.0	358	2	US-09-388-993-1	Sequence 1 Sequence 1	
27	46	63.0	358	2	US-09-991-181-148	•	
				2		Sequence 1	- -
28	46	63.0	358	2	US-09-501-714-1	Sequence 1	
29	46	63.0	358	2	US-09-990-444-148 US-09-997-333-148	Sequence 1	
30	46	63.0	358	_		Sequence 1	
31	46	63.0	358	2	US-09-992-598-148	Sequence 1	
32	46	63.0	358	2	US-09-989-735-148	Sequence 1	
33	46	63.0	358	3	US-09-989-726-148	Sequence 1	
34	46	63.0	358	3	US-09-997-514-148	Sequence 1	
35	46	63.0	358	3	US-09-989-728-148	Sequence 1	
36	46	63.0	358	3	US-09-997-349-148	Sequence 1	
37	46	63.0	358	3	US-09-997-653-148	Sequence 1	
38	46	63.0	358	3	US-09-989-293A-148	Sequence 1	
39	44	60.3	311	2	US-09-248-796A-16958	Sequence 1	
40	43	58.9	147	2	US-09-513-999C-6925	Sequence 6	•
41	42	57.5	138	2	US-09-902-540-13689	Sequence 1	•
42	42	57.5	276	2	US-09-270-767-43364	Sequence 4	-
43	42	57.5	391	2	US-09-902-540-11110	Sequence 1	•
44	41	56.2	254	2	US-09-859-822-2	Sequence 2	• • •
45	41	56.2	373	2	US-09-710-279-890	Sequence 8	
46	41	56.2	385	2	US-09-134-001C-3688	Sequence 3	•
47	41	56.2	514	2	US-09-252-991A-18326	Sequence 1	·
48	40	54.8	95	2	US-09-248-796A-19797	Sequence 1	·
49	40	54.8	145	2	US-09-427-700-9	Sequence 9	
50	40	54.8	146	1	US-07-989-363-2	Sequence 2	
51	40	54.8	146	1	US-08-264-526-2	Sequence 2	
52	40	54.8	320	2	US-09-328-352-7937	Sequence 7	•
53	40	54.8	330	1	US-08-868-288A-3	Sequence 3	• •
54	40	54.8	330	2	US-09-235-373-3	Sequence 3	• •
55	40	54.8	330	2	US-09-388-993-3	Sequence 3	3, Appli
56	40	54.8	330	2	US-09-501-714-3	Sequence 3	
57	40	54.8	376	3	US-10-375-010-22	Sequence 2	
58	40	54.8	422	1	US-08-152-483B-3	Sequence 3	
59	40	54.8	426	1	US-08-152-483B-7	Sequence 7	7, Appli
60	40	54.8	478	1	US-08-152-483B-9	Sequence 9	9, Appli
61	40	54.8	497	2	US-09-328-352-7286	Sequence 7	• -
62	40	54.8	503	2	US-09-562-737-68	Sequence 6	
63	39	53.4	43	2	US-09-209-676-77	Sequence 7	77, Appl

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-9.rapbm.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

June 2, 2006, 19:58:51; Search time 63.3553 Seconds

(without alignments)

109.671 Million cell updates/sec

Title:

US-10-001-938-9

Perfect score: 73

Sequence: 1 ASYYEILDVPRSASA 15

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched:

2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters:

2097797

Minimum DB seg length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA Main:*

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

3: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B PUBCOMB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11 PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No. Score Match Length DB ID

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Description

1	7.2	100 0	1 0	Λ	TTG 10 001 020 0	Carriana O Dani	1 4
1	73 53	100.0	15	4	US-10-001-938-9	Sequence 9, Appl	_
2	52 52	71.2	223	4	US-10-028-072-30	Sequence 30, App	_
3	52	71.2	223	4	US-10-140-808-30	Sequence 30, App	_
4	52	71.2	223	4	US-10-121-049-30	Sequence 30, App	_
5	52	71.2	223	4	US-10-123-904-30	Sequence 30, App	_
6	52	71.2	223	4	US-10-140-470-30	Sequence 30, App	
7	52	71.2	223	4	US-10-175-746-30	Sequence 30, App	•
8	52	71.2	223	4	US-10-176-918-30	Sequence 30, App	21
9	52	71.2	223	4	US-10-176-921-30	Sequence 30, App	21
10	52	71.2	223	4	US-10-137-865-30	Sequence 30, App	pl.
11	52	71.2	223	4	US-10-140-474-30	Sequence 30, App	ol
12	52	71.2	223	4	US-10-142-431-30	Sequence 30, App	21
13	52	71.2	223	4	US-10-143-114-30	Sequence 30, App	ol.
14	52	71.2	223	4	US-10-142-419-30	Sequence 30, App	ol
15	52	71.2	223	4	US-10-123-262-30	Sequence 30, App	
16	52 .	71.2	223	4	US-10-142-423-30	Sequence 30, App	
17	52	71.2	223	4	US-10-121-050-30	Sequence 30, App	
18	52	71.2	223	4	US-10-141-755-30	Sequence 30, App	
19	52	71.2	223	4	US-10-143-032-30	Sequence 30, App	_
20	52	71.2	223	4	US-10-123-108-30	Sequence 30, App	
21	52	71.2	223	4	US-10-123-236-30	Sequence 30, App	
22	52	71.2	223	4	US-10-123-261-30	Sequence 30, App	
23	52	71.2	223	4	US-10-140-921-30	Sequence 30, App	
24	52	71.2	223	4	US-10-140-928-30	Sequence 30, App	
25	52	71.2	223	4	US-10-140-920-30	Sequence 30, App	_
26	52 52	71.2	223	4	US-10-121-045-30 US-10-123-292-30		
27	52 52	71.2	223	4	US-10-123-292-30 US-10-123-903-30	Sequence 30, App Sequence 30, App	
28		71.2	223	4	US-10-124-819-30		_
	52 52	71.2		-	US-10-124-819-30 US-10-124-822-30	Sequence 30, App	_
29	52 52	71.2	223 223	4		Sequence 30, App	_
30	52 52			4	US-10-140-925-30	Sequence 30, App	_
31	52 52	71.2	223	4	US-10-160-498-30	Sequence 30, App	
32	52	71.2	223	4	US-10-124-824-30	Sequence 30, App	_
33	52 52	71.2	223	4	US-10-127-825A-30	Sequence 30, App	_
34	52	71.2	223	4	US-10-127-829A-30	Sequence 30, App	_
35	52	71.2	223	4	US-10-127-835A-30	Sequence 30, App	_
36	52	71.2	223	4	US-10-127-839A-30	Sequence 30, App	_
37	52	71.2	223	4	US-10-127-901A-30	Sequence 30, App	•
38	52	71.2	223	4	US-10-128-693A-30	Sequence 30, App	_
39	52	71.2	223	4	US-10-131-813A-30	Sequence 30, App	_
40	52	71.2	223	4	US-10-131-818A-30	Sequence 30, App	
41	52	71.2	223	4	US-10-131-823A-30	Sequence 30, App	_
42	52	71.2	223	4	US-10-131-824A-30	Sequence 30, App	_
43	52	71.2	223	4	US-10-131-830A-30	Sequence 30, App	_
44	52	71.2	223	4	US-10-131-837A-30	Sequence 30, App	•
45	52	71.2	223	4	US-10-137-872A-30	Sequence 30, App	-
46	52	71.2	223	4	US-10-147-500-30	Sequence 30, App	pl
47	52	71.2	223	4	US-10-147-502-30	Sequence 30, App	pl
48	52	71.2	223	4	US-10-147-515-30	Sequence 30, App	_
49	52	71.2	223	4	US-10-147-517-30	Sequence 30, App	pl
50	52	71.2	223	4	US-10-147-526-30	Sequence 30, App	pl
51	52	71.2	223	4	US-10-147-527-30	Sequence 30, App	pl
52	52	71.2	223	4	US-10-121-041-30	Sequence 30, App	ρl
53	52	71.2	223	4	US-10-121-043-30	Sequence 30, App	pl
54	52	71.2	223	4	US-10-121-047-30	Sequence 30, App	
55	52	71.2	223	4	US-10-123-215-30	Sequence 30, App	pl
56	52	71.2	223	4	US-10-123-902-30	Sequence 30, App	•
57	52	71.2	223	4	US-10-123-908-30	Sequence 30, App	_
58	52	71.2	223	4	US-10-123-909-30	Sequence 30, App	
59	52	71.2	223	4	US-10-123-910-30	Sequence 30, App	
60	52	71.2	223	4	US-10-124-813-30	Sequence 30, App	
61	52	71.2	223	4	US-10-124-817-30	Sequence 30, App	_
						•	

SCORE Search Results Details for Application 10001938 and Search Result us-10-001-938-9.rapbn.

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This page gives you Search Results detail for the Application 10001938 and Search Result us-10-00 938-9.rapbn.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

June 2, 2006, 19:45:07; Search time 3.55263 Seconds Run on:

(without alignments)

48.831 Million cell updates/sec

Title: US-10-001-938-9

Perfect score: 73

1 ASYYEILDVPRSASA 15 Sequence:

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

58871 seqs, 11565156 residues Searched:

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Published Applications AA New: * Database :

/EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07 NEW PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08 NEW PUB.pep:*

5: /EMC Celerra SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10 NEW PUB.pep:*

7: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11 NEW PUB.pep:*

/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

No.	Score	Match	Length	DB	ID	Description
1	73	100.0	15	6	US-10-490-949-18	Sequence 18, Appl
2	51	69.9	161	6	US-10-953-349-37092	Sequence 37092, A
3	51	69.9	190	6	US-10-953-349-37091	Sequence 37091, A
4	41	56.2	419	6	US-10-953-349-1054	Sequence 1054, Ap
5	40	54.8	417	6	US-10-953-349-16377	Sequence 16377, A
6	39	53.4	160	6	US-10-953-349-6860	Sequence 6860, Ap
7	38	52.1	420	6	US-10-953-349-13709	Sequence 13709, A
8	37	50.7	138	6	US-10-953-349-20728	Sequence 20728, A
9	37	50.7	158	6	US-10-953-349-20727	Sequence 20727, A
10	37	50.7	159	6	US-10-953-349-20726	Sequence 20726, A
11	37	50.7	335	6	US-10-953-349-2182	Sequence 2182, Ap
12	37	50.7	336	6	US-10-953-349-33810	Sequence 33810, A
13	37	50.7	343	6	US-10-953-349-2181	Sequence 2181, Ap
14	37	50.7	429	7	US-11-293-697-4865	Sequence 4865, Ap
15	37	50.7	430	6	US-10-953-349-33809	Sequence 33809, A
16	36	49.3	15	6	US-10-490-949-2	Sequence 2, Appli
17	36	49.3	95	6	US-10-953-349-31080	Sequence 31080, A
18	36	49.3	156	6	US-10-953-349-5018	Sequence 5018, Ap
19	36	49.3	230	6	US-10-953-349-18065	Sequence 18065, A
20	36	49.3	230	6	US-10-953-349-18284	Sequence 18284, A
21	36	49.3	234	6	US-10-953-349-18064	Sequence 18064, A
22	36	49.3	234	6	US-10-953-349-18283	Sequence 18283, A
23	36	49.3	259	6	US-10-953-349-18063	Sequence 18063, A
24	36	49.3	259	6	US-10-953-349-18282	Sequence 18282, A
25	36	49.3	397	7	US-11-293-697-3837	Sequence 3837, Ap
26	36	49.3	426	7	US-11-293-697-4751	Sequence 4751, Ap
27	35	47.9	339	6	US-10-953-349-12422	Sequence 12422, A
28	35	47.9	379	6	US-10-953-349-11645	Sequence 11645, A
29	35	47.9	380	6	US-10-953-349-7175	Sequence 7175, Ap
30	35	47.9	380	7	US-11-252-080-10	Sequence 10, Appl
31	35	47.9	389	7	US-11-122-986-185	Sequence 185, App
32	35	47.9	389	7	US-11-122-986-187	Sequence 187, App
33	35	47.9	391	6	US-10-953-349-7174	Sequence 7174, Ap
34	35	47.9	442	6	US-10-953-349-7173	Sequence 7173, Ap
35	35	47.9	458	7	US-11-293-697-3646	Sequence 3646, Ap
36	35	47.9	504	6	US-10-511-937-2547	Sequence 2547, Ap
37	34	46.6	153	6	US-10-953-349-36584	Sequence 36584, A
38	34	46.6	167	6	US-10-953-349-34156	Sequence 34156, A
39	34	46.6	167	6	US-10-953-349-39090	Sequence 39090, A
40	34	46.6	179	6	US-10-953-349-36583	Sequence 36583, A
41	34	46.6	233	6	US-10-953-349-9315	Sequence 9315, Ap
42	34	46.6	233	6	US-10-953-349-12246	Sequence 12246, A
43	34	46.6	233	6	US-10-953-349-21982	Sequence 21982, A
44	34	46.6	234	6	US-10-953-349-6532	Sequence 6532, Ap
45	34	46.6	235	6	US-10-953-349-30723	Sequence 30723, A
46	34	46.6	237	6	US-10-953-349-39891	Sequence 39891, A
47	34	46.6	238	6	US-10-953-349-335	Sequence 335, App
48	34	46.6	238	6	US-10-953-349-6531	Sequence 6531, Ap
49	34	46.6	242	6	US-10-953-349-334	Sequence 334, App
50	34	46.6	246	6	US-10-953-349-9314	Sequence 9314, Ap
51	34	46.6	246	6	US-10-953-349-12245	Sequence 12245, A
52	34	46.6	246	6	US-10-953-349-21981	Sequence 21981, A
53	34	46.6	248	6	US-10-953-349-30722	Sequence 30722, A
54	34	46.6	250	6	US-10-953-349-39890	Sequence 39890, A
55	34	46.6	253	6	US-10-953-349-5910	Sequence 5910, Ap
56	34	46.6	255	6	US-10-953-349-9313	Sequence 9313, Ap
57	34	46.6	257	6	US-10-953-349-12244	Sequence 12244, A
58	34	46.6	259	6	US-10-953-349-21980	Sequence 21980, A
59	34	46.6	260	6	US-10-953-349-39889	Sequence 39889, A